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OM protein - protein search, using sw model

Run on: January 12, 2003, 01:54:58 ; Search time 69 Seconds

(without alignments)  
27.036 Million cell updates/sec

Title: HANDENTERED

Perfect score: 70

Sequence: 1 supprek1p1slk 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08

Maximum Match 1008

Listing first 45 summaries

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3: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*
4: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*
5: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*
6: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*
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8: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*
9: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*
10: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*
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13: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*
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15: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*
16: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*
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19: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*
20: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*
21: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*
22: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*
23: /SIDS2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	70	100.0	14	AA11461	Human brain carbox
2	70	100.0	246	AA11459	Human brain carbox
3	70	100.0	338	AA11458	Human brain carbox
4	70	100.0	360	AA11457	Human brain carbox
5	42	60.0	403	AA11457	Human brain carbox
6	42	60.0	431	AA11457	Human brain carbox
7	42	60.0	450	AA11457	Human brain carbox
8	42	60.0	450	AA11457	Human brain carbox
9	42	60.0	1544	AA11457	Human brain carbox
10	41	58.6	2681	AA11457	Human brain carbox

11	40	57.1	48	22	AA102560
12	40	57.1	105	21	AA104086
13	40	57.1	412	21	AA107823
14	40	57.1	904	23	AA108077
15	39	55.7	48	22	AA108640
16	39	55.7	52	22	AA108640
17	39	55.7	57	21	AA108640
18	39	55.7	58	21	AA108640
19	39	55.7	89	20	AA108640
20	39	55.7	103	22	AA108640
21	39	55.7	111	22	AA108640
22	39	55.7	230	22	AA108640
23	39	55.7	255	22	AA108640
24	39	55.7	278	22	AA108640
25	39	55.7	307	22	AA108640
26	39	55.7	317	22	AA108640
27	39	55.7	317	22	AA108640
28	39	55.7	322	21	AA108640
29	39	55.7	331	22	AA108640
30	39	55.7	442	22	AA108640
31	39	55.7	653	17	AA108640
32	39	55.7	992	22	AA108640
33	38	54.3	67	23	AA108640
34	38	54.3	69	20	AA108640
35	38	54.3	106	23	AA108640
36	38	54.3	219	23	AA108640
37	38	54.3	221	21	AA108640
38	38	54.3	282	22	AA108640
39	38	54.3	292	22	AA108640
40	38	54.3	348	21	AA108640
41	38	54.3	348	21	AA108640
42	38	54.3	359	23	AA108640
43	38	54.3	371	21	AA108640
44	38	54.3	371	21	AA108640
45	38	54.3	388	22	AA108640

#### ALIGNMENTS

```
RESULT 1
ID AA11461 standard; Protein: 14 AA.
AC AA11461;
XX
XX 01-MAR-2001 (first entry)
DT
XX
XX Human brain carboxypeptidase B protein SEQ ID NO 9.
DE
XX Carboxypeptidase B; human; brain; hippocampus; APP cleavage; peptidase;
XX treatment; Alzheimer's disease; beta-amyloid precursor protein; vaccine;
XX cerebroprotective; antialzheimer's; neurotrophic; neuroprotective;
XX hemostatic; gene therapy; senile dementia; inherited cerebral hemorrhage;
XX Down's syndrome; head trauma.
OS
XX Homo sapiens.
XX
XX WO200066717-A1.
XX
XX 09-NOV-2000.
XX
XX 01-MAY-2000; 2000WO-JP02878.
XX
XX 30-APR-1999; 99JP-0125169.
XX
XX (MATS/) MATSUMOTO A.
XX
XX Matsumoto A;
XX
XX WPI: 2000-687534/67.
XX
XX Human brain carboxypeptidase B isolated from the hippocampus useful for
```

PT screening agents for the treatment of Alzheimer's and other brain  
PT disorders -  
XX  
PS Example 4; Page 78; 84pp; Japanese.  
XX  
CC This invention describes a novel protein with peptidase activity  
CC against brain beta-amyloid precursor protein which has been isolated from  
CC human hippocampus and which has cerebroprotective, antialzheimers,  
CC neurotropic, neuroprotective and hemostatic activity, and which can be used  
CC as a vaccine or for gene therapy. The protein, and compounds identified  
CC by screening as promoters or inhibitors of its activity, are used to  
CC regulate beta-amyloid accumulation in the brain and treat or prevent  
CC diseases in which this occurs, such as Alzheimer's, senile dementia,  
CC inherited cerebral hemorrhage, Down's syndrome, and head trauma.  
XX  
SQ Sequence 14 AA;  
XX  
Query Match 100.0%; Score 70; DB 21; Length 14;  
Best Local Similarity 100.0%; Pred. No. 3.9e-05;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SNPEVKLPLSLK 14  
Db 1 SNPEVKLPLSLK 14  
DE  
RESULT 2  
ID AAB11459  
AC AAB11459; standard; Protein; 246 AA.  
XX  
AC AAB11459;  
XX  
DT 01-MAR-2001 (first entry)  
XX  
DE Human brain carboxypeptidase B protein SEQ ID NO 4.  
XX  
KW Carboxypeptidase B; human; brain; hippocampus; APP cleavage; peptidase;  
KW treatment; Alzheimer's disease; beta-amyloid precursor protein; vaccine;  
KW cerebroprotective; antialzheimers; neurotropic; neuroprotective;  
KW hemostatic; gene therapy; senile dementia; inherited cerebral hemorrhage;  
KW Down's syndrome; head trauma.  
XX  
PI Matsumoto A;  
XX  
OS Homo sapiens.  
XX  
PN WO200066717-A1.  
XX  
PD 09-NOV-2000.  
XX  
PE 01-MAY-2000; 2000MO-JP02878.  
XX  
PS 30-APR-1999; 99JP-0125169.  
XX  
PA (MATS/) MATSUMOTO A.  
XX  
PI Matsumoto A;  
XX  
PI WPI; 2000-687534/67.  
XX  
PT Human brain carboxypeptidase B isolated from the hippocampus useful for  
PT screening agents for the treatment of Alzheimer's and other brain  
PT disorders -  
XX  
PS Disclosure; Page 74-75; 84pp; Japanese.  
XX  
CC This invention describes a novel protein with peptidase activity  
CC against brain beta-amyloid precursor protein which has been isolated from  
CC human hippocampus and which has cerebroprotective, antialzheimers,  
CC neurotropic, neuroprotective and hemostatic activity, and which can be used  
CC as a vaccine or for gene therapy. The protein, and compounds identified  
CC by screening as promoters or inhibitors of its activity, are used to  
CC regulate beta-amyloid accumulation in the brain and treat or prevent  
CC diseases in which this occurs, such as Alzheimer's, senile dementia,  
CC inherited cerebral hemorrhage, Down's syndrome, and head trauma.

XX  
SQ Sequence 246 AA;  
XX  
Query Match 100.0%; Score 70; DB 21; Length 246;  
Best Local Similarity 100.0%; Pred. No. 0.00095;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SNPEVKLPLSLK 14  
Db 233 SNPEVKLPLSLK 246  
DE  
RESULT 3  
ID AAB11458  
AC AAB11458; standard; Protein; 338 AA.  
XX  
AC AAB11458;  
XX  
DT 01-MAR-2001 (first entry)  
XX  
DE Human brain carboxypeptidase B protein SEQ ID NO 3.  
XX  
KW Carboxypeptidase B; human; brain; hippocampus; APP cleavage; peptidase;  
KW treatment; Alzheimer's disease; beta-amyloid precursor protein; vaccine;  
KW cerebroprotective; antialzheimers; neurotropic; neuroprotective;  
KW hemostatic; gene therapy; senile dementia; inherited cerebral hemorrhage;  
KW Down's syndrome; head trauma.  
XX  
PI Matsumoto A;  
XX  
OS Homo sapiens.  
XX  
PN WO200066717-A1.  
XX  
PD 09-NOV-2000.  
XX  
PE 01-MAY-2000; 2000MO-JP02878.  
XX  
PS 30-APR-1999; 99JP-0125169.  
XX  
PA (MATS/) MATSUMOTO A.  
XX  
PI Matsumoto A;  
XX  
PI WPI; 2000-687534/67.  
XX  
PT Human brain carboxypeptidase B isolated from the hippocampus useful for  
PT screening agents for the treatment of Alzheimer's and other brain  
PT disorders -  
XX  
PS Disclosure; Page 71-73; 84pp; Japanese.  
XX  
CC This invention describes a novel protein with peptidase activity  
CC against brain beta-amyloid precursor protein which has been isolated from  
CC human hippocampus and which has cerebroprotective, antialzheimers,  
CC neurotropic, neuroprotective and hemostatic activity, and which can be used  
CC as a vaccine or for gene therapy. The protein, and compounds identified  
CC by screening as promoters or inhibitors of its activity, are used to  
CC regulate beta-amyloid accumulation in the brain and treat or prevent  
CC diseases in which this occurs, such as Alzheimer's, senile dementia,  
CC inherited cerebral hemorrhage, Down's syndrome, and head trauma.  
XX  
SQ Sequence 338 AA;  
XX  
Query Match 100.0%; Score 70; DB 21; Length 338;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 SNPEVKLPLSLK 14  
Db 325 SNPEVKLPLSLK 338  
DE  
RESULT 4  
ID AAB11457

ID	AA01457 standard; Protein: 360 AA.
AC	AA01457;
DT	01-MAR-2001 (first entry)
XX	
DE	Human brain carboxypeptidase B protein.
XX	
KW	Carboxypeptidase B; human; brain; hippocampus; APP cleavage; peptidase; treatment; Alzheimer's disease; beta-amyloid precursor protein; vaccine; cerebroprotective; antialzheimer's; neurotrophic; neuroprotective; KW hemostatic; gene therapy; senile dementia; inherited cerebral hemorrhage; XX Down's syndrome; head trauma.
OS	Homo sapiens.
PN	MO200066717-A1.
PD	09-NOV-2000.
XX	
PE	01-MAY-2000; 2000WO-JP02878.
XX	
PR	30-APR-1999; 99JP-0125169.
XX	
PA	(MATS/) MATSUMOTO A.
PI	Matsumoto A;
DR	MPI: 2000-687534/67.
XX	N-PSDB; NAC81962.
PT	Human brain carboxypeptidase B isolated from the hippocampus useful for screening agents for the treatment of Alzheimer's and other brain disorders -
XX	
PS	Claim 1; Page 68-71; 84pp; Japanese.
CC	This invention describes a novel protein with peptidase activity against brain beta-amyloid precursor protein which has been isolated from human hippocampus and which has cerebroprotective, antialzheimer's, neurotrophic, neuroprotective and hemostatic activity and which can be used as a vaccine or for gene therapy. The protein, and compounds identified by screening beta-amyloid accumulation in the brain and treat or prevent diseases in which this occurs, such as Alzheimer's, senile dementia, inherited cerebral hemorrhage, Down's syndrome, and head trauma.
SQ	Sequence 360 AA;
Query Match	100.0%; Score 70; DB 21; Length 360;
Best Local Similarity	100.0%; Pred. NO. 0.0015;
Matches 14; Conservative	0; Mismatches 0; Indels 0; Gaps 0
OY	1 SNPPVEKLLPLSLK 14 
Db	347 SNPPVEKLLPLSLK 360
RESULT 5	
AAB94027	
ID	AAB94027 standard; Protein: 403 AA.
XX	
AC	AAB94027;
DT	26-JUN-2001 (first entry)
XX	
DE	Human protein sequence SEQ ID NO:14166.
XX	
KW	Human; primer; detection; diagnosis; antisense therapy; gene therapy.
OS	Homo sapiens.
XX	
PN	EP1074617-A2.

XX	07-FEB-2001.
PD	
PF	28-JUL-2000; 2000EP-0116126.
XX	
PR	29-JUL-1999; 99JP-0248036.
PR	27-AUG-1999; 99JP-0300253.
PR	11-JAN-2000; 2000JP-0118776.
PR	02-MAY-2000; 2000JP-0183767.
PR	09-JUN-2000; 2000JP-0241899.
XX	
PA	(HELI-) HELIX RES INST.
XI	
PI	Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
PI	Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX	
DR	WPI; 2001-318749/34.
XX	
PT	Primer sets for synthesizing polynucleotides, particularly the 5602
PT	full-length cDNAs defined in the specification, and for the detection
PT	and/or diagnosis of the abnormality of the proteins encoded by the
PT	full-length cDNAs -
PS	
XX	Claim 8; SEQ ID 14166; 2537/gp + CD ROM; English.
XX	
CC	The present invention describes primer sets for synthesizing 5602
CC	full-length cDNAs defined in the specification, where a primer set
CC	comprises: (a) an oligo-dT primer and an oligonucleotide complementary
CC	to the complementary strand of a polynucleotide which comprises one of
CC	the 5602 nucleotide sequences defined in the specification, where the
CC	oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC	of an oligonucleotide comprising a sequence complementary to the
CC	complementary strand of a polynucleotide which comprises a 5'-end
CC	sequence and an oligonucleotide comprising a sequence complementary to a
CC	polynucleotide which comprises a 3'-end sequence, where the
CC	oligonucleotide comprises at least 15 nucleotides and the combination of
CC	the 5'-end sequence/3'-end sequence is selected from those defined in
CC	the specification. The primer sets can be used in antisense therapy and
CC	in gene therapy. The primers are useful for synthesizing polynucleotides,
CC	particularly full-length cDNAs. The primers are also useful for the
CC	detection and/or diagnosis of the abnormality of the proteins encoded by
CC	the full-length cDNAs. The primers allow obtaining of the full-length
CC	cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC	AAH13633 to AAH18742 represent human cDNA sequences; AAH92446 to
CC	AAH95893 represent human amino acid sequences; and AAH13629 to AAH13632
CC	represent oligonucleotides, all of which are used in the exemplification
CC	of the present invention.
XX	
SQ	Sequence 403 AA:
QY	
DB	86 PPLEKILPL 94
XX	
XX	Query Match . 60.0%; Score 42; DB 22; Length 403;
XX	Best Local Similarity 77.8%; Pred. No. 79;
XX	Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0
XX	
XX	3 PVEKLPL 11
XX	
ID	AAV86203 standard; Protein; 431 AA.
AC	AAV86203;
DT	11-APR-2000 (first entry)
DE	Nuclear transport protein clone hFB2060 protein sequence.
KX	Nuclear transport protein; drug delivery system; visual detection; human;
KM	nuclear transport indicator.
OS	Homo sapiens.

XX PN W09964455-A1.  
 XX PD 16-DEC-1999.  
 XX PF 04-JUN-1999; 99WO-JP03015.  
 XX PR 05-JUN-1998; 98JP-0174065.  
 XX PR 14-APR-1999; 99JP-0107262.  
 XX PA (HELI-) HELIX RES INST.  
 XX PI Ueki N, Yano K;  
 XX DR WPI; 2000-105872/09.  
 XX DR N-PSDB; AA296761.  
 XX PT Peptides with nuclear transport activity, applicable as carrier for  
 XX PT transport desirable substances, e.g. drugs into nucleus, and as nuclear  
 XX PT transport indicators after modification for visual detection  
 XX PS Claim 1; Page 84-87; 309pp; Japanese.  
 CC This sequence represents the amino acid sequence of a nuclear transport  
 CC protein of the invention. The invention relates to peptides with nuclear  
 CC transport activity, and also includes similar peptides with the same  
 CC transport activity, but with some amino acids deleted, substituted and/or  
 CC added. The peptides can be used as carriers for transferring desirable  
 CC substances particularly drugs, including nucleic acids and proteins, into  
 CC the nucleus in a drug delivery system. The peptides can also be used as  
 CC nuclear transport indicators after modification for visual detection.  
 CC Drugs can be delivered efficiently with the peptides to a specific target  
 CC site. This delivery allows the maintenance of drug concentration,  
 CC therapeutic efficacy and a reduction of side-effects of such drugs to be  
 CC achieved.  
 XX SQ Sequence 431 AA;  
 Query Match 60.0%; Score 42; DB 21; Length 431;  
 Best Local Similarity 77.8%; Pred. No. 86;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 PPVEKILPL 11  
 DB 147 PPVEKILPL 155  
 RESULT 7  
 ABB91564  
 ID ABB91564 standard; Protein: 450 AA.  
 XX AC ABB91564;  
 XX DT 31-MAY-2002 (first entry)  
 DE Herbicidally active polypeptide SEQ ID NO 775.  
 KW Herbicidally active polypeptide; herbicide.  
 XX OS Arabidopsis thaliana.  
 XX PN W0200210210-A2.  
 XX PD 07-FEB-2002.  
 XX PF 28-AUG-2001; 2001WO-EP09892.  
 XX PR 28-AUG-2001; 2001WO-EP09892.  
 XX PA (FARB ) BAYER AG.  
 XX PI Tietjen K, Weidner M;  
 XX

DR WPI; 2002-269010/31.  
 XX Identifying plant target proteins for herbicidally active compounds,  
 PT comprising aligning and comparing nucleic acid or amino acid sequences  
 PT from plant with nucleic acid or amino acid sequences from non-plant  
 PT organisms -  
 XX PS Claim 5; SEQ ID NO 775; 261pp + Sequence Listing; English.  
 CC The invention relates to identifying target proteins  
 CC (ABB90790-ABB94016) for herbicidally active compounds, comprising  
 CC aligning and comparing nucleic acid or amino acid sequences from plant  
 CC with nucleic acid or amino acid sequences from non-plant organisms using  
 CC suitable search parameters, where plant sequences having an E-value  
 CC greater by a factor of 3 than the E-value of most similar non-plant  
 CC sequences are selected. The polypeptides or nucleic acids encoding them  
 CC are useful for identifying modulators. The identified modulators are  
 CC useful as herbicides.  
 XX SQ Sequence 450 AA;  
 Query Match 60.0%; Score 42; DB 23; Length 450;  
 Best Local Similarity 75.0%; Pred. No. 90;  
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 SNPPVEKILPL 12  
 DB 26 TNPPEKILPL 37  
 RESULT 8  
 AAB94063  
 ID AAB94063 standard; Protein: 1038 AA.  
 XX AC AAB94063;  
 XX DT 26-JUN-2001 (first entry)  
 DE Human protein sequence SEQ ID NO:14242.  
 XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.  
 XX OS Homo sapiens.  
 XX PN EP1074617-A2.  
 XX PD 07-FEB-2001.  
 XX PF 28-JUL-2000; 2000EP-0116126.  
 XX PR 29-JUL-1999; 99JP-0248036.  
 XX PR 27-AUG-1999; 99JP-0300253.  
 XX PR 11-JAN-2000; 2000JP-0118776.  
 XX PR 02-MAY-2000; 2000JP-0183767.  
 XX PR 09-JUN-2000; 2000JP-0241899.  
 XX PA (HELI-) HELIX RES INST.  
 XX PI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;  
 XX PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;  
 XX DR WPI; 2001-318749/34.  
 XX PT Primer sets for synthesizing polynucleotides, particularly the 5602  
 PT full-length cDNAs defined in the specification, and for the detection  
 PT and/or diagnosis of the abnormality of the proteins encoded by the  
 PT full-length cDNAs -  
 XX PS Claim 8; SEQ ID 14242; 2537pp + CD ROM; English.  
 CC The present invention describes primer sets for synthesizing 5602  
 CC full-length cDNAs defined in the specification. Where a primer set  
 CC comprises: (a) an oligo-dt primer and an oligonucleotide complementary

CC to the complementary strand of a polynucleotide which comprises one of  
 CC the 5602 nucleotide sequences defined in the specification, where the  
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination  
 CC of an oligonucleotide comprising a sequence complementary to the  
 CC complementary strand of a polynucleotide which comprises a 5'-end  
 CC sequence and an oligonucleotide comprising a sequence complementary to a  
 CC polynucleotide which comprises a 3'-end sequence, where the  
 CC oligonucleotide comprises at least 15 nucleotides and the combination of  
 CC the 5'-end sequence/3'-end sequence is selected from those defined in  
 CC the specification. The primer sets can be used in antisense therapy and  
 CC in gene therapy. The primers are useful for synthesizing polynucleotides,  
 CC particularly full-length cDNAs. The primers are also useful for the  
 CC detection and/or diagnosis of the abnormality of the proteins encoded by  
 CC the full-length cDNAs. The primers allow obtaining of the full-length  
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and  
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to  
 CC AAB95893 represent human amino acid sequences; and AAH13629 to AAH13632  
 CC represent oligonucleotides, all of which are used in the exemplification  
 CC of the present invention.

SQ Sequence 1038 AA;

Query Match 60.0%; Score 42; DB 22; Length 1038;  
 Best Local Similarity 77.8%; Pred. No. 2.3e+02;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 PPEVKLLPL 11  
 11:11:111  
 DB 832 PPLEKILPL 840

RESULT 9  
 AAY41109  
 ID AAY41109 standard; Protein; 1544 AA.

AC AAY41109;

DT 17-JAN-2000 (first entry)

DE Human cancer-associated polypeptide plu-1.

KM Human; cancer-associated polypeptide; plu-1; ovarian cancer; vaccine;  
 breast cancer; immune response; cytotoxic T lymphocyte; imaging agent;  
 therapeutic; plu-1 antigen; breast tumor; tumor antigen.

OS Homo sapiens.

PN WO9949034-A1.

PD 30-SEP-1999.

PF 19-MAR-1999; 99WO-GB00866.

PR 20-MAR-1998; 98GB-0005877.

PA (IMCR ) IMPERIAL CANCER RES TECHNOLOGY.

PI Taylor-papadimitriou J;

DR WPI: 1999-591090/50.

DR N-PSDB: AA23079.

PT New nucleic acid encoding the cancer-associated polypeptide plu-1, for  
 PT diagnosis, treatment and prevention of cancer, especially of breast and  
 PT ovary

PS Claim 11; Fig 2; 173pp; English.

CC This represents a human cancer-associated polypeptide plu-1. The plu-1  
 CC polypeptide can be recombinantly expressed by standard recombinant  
 CC methodology. Detection of the plu-1 nucleic acid or the polypeptide is  
 CC used for the following: (i) diagnosis (including imaging) and prognosis  
 CC of, and determination of susceptibility to, cancer, specifically ovarian

CC or breast cancer; and (i) treating cancer (by inducing an immune response  
 CC against cancer cells, e.g. as a vaccine, or by antisense inhibition).  
 CC Antigens derived from the polypeptide are used to generate activated  
 CC cytotoxic T lymphocytes, or dendritic cells, for subsequent return to the  
 CC patient for treatment of cancer. The polypeptide may also be used to  
 CC identify inhibitors of plu-1 activity. Fragments of the polypeptide, and  
 CC antibodies raised against plu-1, are useful as assay and imaging agents,  
 CC also therapeutically (to induce an anti-idiotypic response or where  
 CC conjugated to cytotoxic agents). The plu-1 antigen is expressed more  
 CC commonly in breast tumors than some known tumor antigens.

SQ Sequence 1544 AA;

Query Match 60.0%; Score 42; DB 20; Length 1544;  
 Best Local Similarity 77.8%; Pred. No. 3.5e+02;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 PPEVKLLPL 11  
 11:11:111  
 DB 1227 PPLEKILPL 1235

RESULT 10  
 ABG29184  
 ID ABG29184 standard; Protein; 2681 AA.

AC ABG29184;

DT 13-FEB-2002 (first entry)

DE Novel human diagnostic protein #29175.

KM Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 food supplement; medical imaging; diagnostic; genetic disorder.

OS Homo sapiens.

PN WO200175067-A2.

PD 11-OCT-2001.

PF 30-MAR-2001; 2001WO-US08631.

PR 31-MAR-2000; 2000US-0540217.

PR 23-AUG-2000; 2000US-0649167.

PA (HYSE-) HYSEQ INC.

PI Drmanac RT, Liu C, Tang YF;

DR WPI: 2001-639362/73.

DR N-PSDB: AAS93371.

PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity

PS Claim 20; SEQ ID No 59543; 103pp; English.

CC The invention relates to isolated polynucleotide (i) and  
 CC polypeptide (ii) sequences. (i) is useful as hybridisation probes,  
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome  
 CC and gene mapping, and in recombinant production of (ii). The  
 CC polynucleotides are also used in diagnostics as expressed sequence tags  
 CC for identifying expressed genes. (ii) is useful in gene therapy techniques  
 CC to restore normal activity of (ii) or to treat disease states involving  
 CC (ii). (ii) is useful for generating antibodies against it, detecting or  
 CC quantitating a polypeptide in tissue, as molecular weight markers and as  
 CC a food supplement. (ii) and its binding partners are useful in medical  
 CC imaging of sites expressing (ii). (i) and (ii) are useful for treating  
 CC disorders involving aberrant protein expression or biological activity.  
 CC The polypeptide and polynucleotide sequences have applications in

CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. ABG00010-ABG30377 represent novel human  
 CC diagnostic amino acid sequences of the invention.  
 CC Note: The sequence data for this patent did not appear in the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 2681 AA;  
 OY 3 PPERKLPUS 12  
 |||||:  
 Db 171 PMEKVIRIS 180  
 Query Match 58.6%; Score 41; DB 22; Length 2681;  
 Best Local Similarity 60.0%; Pred. No. 9.6e+02;  
 Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
 RESULT 11  
 ID AAM82560  
 AAM82560 standard; Protein: 48 AA.  
 AC AAM82560;  
 DT 07-NOV-2001 (first entry)  
 XX  
 DE Human immune/haematopoietic antigen SEQ ID NO:10153.  
 XX  
 KW Human; Immune; haematopoietic; Immune/haematopoietic antigen; cancer;  
 KM cytosolic; gene therapy; vaccine; metastasis.  
 OS Homo sapiens.  
 XX  
 PN WO200157182-A2.  
 PD 09-AUG-2001.  
 PF 17-JAN-2001; 2001WO-US01354.  
 XX  
 PR 31-JAN-2000; 2000US-0179065.  
 PR 04-FEB-2000; 2000US-0180628.  
 PR 24-FEB-2000; 2000US-0184664.  
 PR 02-MAR-2000; 2000US-0186350.  
 PR 16-MAR-2000; 2000US-0189874.  
 PR 17-MAR-2000; 2000US-0190076.  
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 PR 19-MAY-2000; 2000US-0205515.  
 PR 07-JUN-2000; 2000US-0209467.  
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 PR 14-AUG-2000; 2000US-0225757.  
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 PR 29-SEP-2000; 2000US-0236368.  
 PR 29-SEP-2000; 2000US-0236369.  
 PR 29-SEP-2000; 2000US-0236370.  
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 PR 02-OCT-2000; 2000US-0237037.  
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 PR 02-OCT-2000; 2000US-0237039.  
 PR 02-OCT-2000; 2000US-0237040.  
 PR 13-OCT-2000; 2000US-0239935.  
 PR 13-OCT-2000; 2000US-0239937.  
 PR 20-OCT-2000; 2000US-0240960.  
 PR 20-OCT-2000; 2000US-0241221.  
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 PR 20-OCT-2000; 2000US-0241786.  
 PR 20-OCT-2000; 2000US-0241787.  
 PR 20-OCT-2000; 2000US-0241808.  
 PR 20-OCT-2000; 2000US-0241809.  
 PR 20-OCT-2000; 2000US-0241826.  
 PR 01-NOV-2000; 2000US-0244617.  
 PR 08-NOV-2000; 2000US-0246474.  
 PR 08-NOV-2000; 2000US-0246475.  
 PR 08-NOV-2000; 2000US-0246476.  
 PR 08-NOV-2000; 2000US-0246477.  
 PR 08-NOV-2000; 2000US-0246478.  
 PR 08-NOV-2000; 2000US-0246523.  
 PR 08-NOV-2000; 2000US-0246524.  
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 PR 08-NOV-2000; 2000US-0246526.  
 PR 08-NOV-2000; 2000US-0246527.  
 PR 08-NOV-2000; 2000US-0246527.  
 PR 08-NOV-2000; 2000US-0246532.  
 PR 08-NOV-2000; 2000US-0246532.  
 PR 08-NOV-2000; 2000US-0246609.  
 PR 08-NOV-2000; 2000US-0246610.  
 PR 08-NOV-2000; 2000US-0246611.  
 PR 08-NOV-2000; 2000US-0246613.  
 PR 17-NOV-2000; 2000US-0249207.

PR 17-NOV-2000; 2000US-0249208.  
PR 17-NOV-2000; 2000US-0249209.  
PR 17-NOV-2000; 2000US-0249210.  
PR 17-NOV-2000; 2000US-0249211.  
PR 17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250160.  
PR 01-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251868.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
XX  
XX  
PA (HDMA-) HUMAN GENOME SCI INC.  
PI Rosen CA, Barash SC, Ruben SM;  
XX  
XX MPI: 2001-483426/52.  
DR N-PSDB; AAK53341.  
DR  
XX  
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
PT useful for preventing, diagnosing and/or treating cancers and  
PT metastasis -  
PT  
XX  
XX Claim 11: SEQ ID NO 10153; 3071bp + Sequence Listing; English.  
PS  
XX  
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)  
CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic  
CC activity, and can be used in gene therapy and vaccine production. (I)  
CC proteins and polynucleotides may be used in the prevention, diagnosis and  
CC treatment of diseases associated with inappropriate (I) expression. For  
CC example, they may be used to treat disorders associated with decreased  
CC expression by rectifying mutations or deletions in a patient's genome  
CC that affect the activity of (I) by expressing inactive proteins or to  
CC supplement the patient's own production of (I). Additionally, (I)  
CC polynucleotides may be used to produce the secreted (I), by inserting  
CC the nucleic acids into a host cell and culturing the cell to express the  
CC protein. (I) proteins and polynucleotides may be used to prevent,  
CC diagnose and treat immune/hematopoietic-related diseases, especially  
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703  
CC to AAK67694 represent human immune/hematopoietic antigen genomic  
CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169  
CC represent sequences used in the exemplification of the present invention.  
XX  
XX  
SQ Sequence 48 AA:  
Query Match 57 1%; Score 40; DB 22; Length 48;  
Best Local Similarity 70.0%; Pred. No. 16;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 12  
AAB40486  
ID AAB40486 standard; Protein; 105 AA.  
XX  
XX  
AC AAB40486;  
XX  
XX  
DT 08-FEB-2001 (first entry)  
XX  
XX  
DE Human ORFX ORF250 polypeptide sequence SEQ ID NO:500.  
XX  
XX  
KW Human: open reading frame; ORFX: detection; cytostatic; hepatotropic;  
KW vulnery; antiproliferative; antiparkinsonian; neurotrophic; neuroprotective;  
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;  
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;  
KW antiviral; antibacterial; antifungal; antirheumatic; antihypoid;  
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;  
KW neurodegenerative disease; osteoarthritis; graft vs host disease;  
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
KW cholesterol ester storage; systemic lupus erythematosus; infection;  
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
KW bone damage; cartilage damage; antinflammatory disease; coagulation;  
KW thrombosis; contraceptive.  
XX  
XX Homo sapiens.  
XX  
XX MO200058473-A2.  
XX  
XX  
PD 05-OCT-2000.  
XX  
XX  
XX 31-MAR-2000; 2000WO-US08621.  
XX  
XX  
XX 31-MAR-1999; 99US-0127607.  
PR 02-APR-1999; 99US-0127636.  
PR 05-APR-1999; 99US-0127728.  
PR 30-MAR-2000; 2000US-0540763.  
XX  
XX  
PA (CURA-) CURAGEN CORP.  
XX  
XX  
PI Shinkets RA, Leach M;  
XX  
XX MPI: 2000-602362/57.  
DR N-PSDB; AAC74695.  
XX  
XX  
XX Novel nucleic acids and peptides derived from open reading frame X,  
PT useful for treating e.g. cancers, proliferative disorders,  
PT neurodegenerative disorders and cardiovascular disease -  
PT  
XX  
XX  
XX Claim 11; Page 677-678; 5507bp; English.  
XX  
XX  
XX AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,  
CC which represent the human ORFX open reading frames 1 to 3161. The ORFX  
CC sequences have activities such as: cytostatic; hepatotropic; vulnery;  
CC antiproliferative; antiparkinsonian; neurotrophic; neuroprotective;  
CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;  
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;  
CC antidiabetic; hypotensive; dermatological; immunosuppressive;  
CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;  
CC antihypoid; and antianaemic. The sequences can be used for determining  
CC the presence of or predisposition to, or preventing or treating  
CC pathological conditions associated with an ORFX-associated disorder. The  
CC nucleic acids can be used to express ORFX proteins in gene therapy  
CC vectors. The proteins and nucleic acids may be used to treat cancers,  
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,  
CC graft vs host disease, cardiovascular disease, diabetes mellitus,  
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus  
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,  
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,  
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,  
CC nocturnal haemoglobinuria, antinflammatory disease; to enhance  
CC coagulation; to inhibit thrombosis; and as a contraceptive.

XX Sequence 105 AA;  
SQ  
Query Match 57.1%; Score 40; DB 21; Length 105;  
Best Local Similarity 80.0%; Pred. NO. 39;  
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 SNPEVKLPLP 10  
|||||  
DB 40 SNPEVKLPLP 49

RESULT 13  
AA97823  
ID AA97823 standard; Protein: 412 AA.

XX AC AA97823;  
XX DT 29-AUG-2000 (first entry)  
XX DE Pseudomonas sp. WF505 ORF6-6 protein, SEQ ID NO:11.  
XX KW Benzochlorophene oxidase; bco gene cluster; desulphurisation; crude oil;  
XX KM decontamination.  
XX OS Pseudomonas sp. WF505.  
XX PN JP2000093180-A.  
XX PD 04-APR-2000.  
XX PF 28-SEP-1998; 98JP-0272744.  
XX PR 28-SEP-1998; 98JP-0272744.  
XX PA (TOFU) TONEN CORP.  
XX DR WPI: 2000-378972/33.  
XX N-PSDB: AAA38394.

XX PT New proteins useful for desulfurization of crude oil have ability to  
XX control expression of benzochlorophene oxidase group -  
XX Example 1; Page 24-25; 43pp; Japanese.  
XX PS  
XX CC The invention relates to proteins encoded by the benzochlorophene oxidase  
XX (bco) gene cluster from Pseudomonas sp. WF505, specifically the protein  
XX which controls expression of the gene cluster (AA97823), the  
XX benzochlorophene oxidase (bco) enzyme itself (AA97823) and a  
XX benzochlorophene oxidase co-enzyme (AA97824), which controls  
XX benzochlorophene activity via redox regulation. These enzymes are  
XX respectively encoded by the bco gene cluster open reading frames ORF2-16  
XX (AAA38398), ORF4-9 (AAA38396) and ORF6-7 (AAA38395). The invention also  
XX encompasses genetic constructs and vectors comprising the genes encoding  
XX these proteins, hosts containing such constructs and the recombinant  
XX production of the enzymes. Pseudomonas sp. WF505 benzochlorophene oxidase,  
XX benzochlorophene oxidase co-enzyme and bco gene cluster regulator are  
XX useful in the desulfurization of crude oil and petroleum products, and  
XX for the clarification of soil and waste water contaminated by organic  
XX sulphur compounds. Sequences AA97819-197829 represent the proteins  
XX encoded by the genes of the Pseudomonas sp. WF505 benzochlorophene oxidase  
XX gene cluster.  
XX SQ Sequence 412 AA;

Query Match 57.1%; Score 40; DB 21; Length 412;  
Best Local Similarity 58.3%; Pred. NO. 1.8e+02;  
Matches 7; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNPEVKLPLP 12  
||||| :||:|  
DB 297 SNPEVKLPLP 308

RESULT 14  
ABB80607  
ID ABB80607 standard; Protein: 904 AA.  
XX AC ABB80607;  
XX DT 08-OCT-2002 (first entry)  
XX DE Human sbg1016951GBrecept protein #1.  
XX KW Human; secreted protein; immunosuppressive; cytostatic; nootropic;  
KW neuroprotective; antitumor; vulnery; antineoplastic; ophthalmological;  
KW antiparkinsonian; antihypertensive; antidiabetic; dermatological;  
KW hypotensive; cerebroprotective; virucide; antineoplastic; diabetes;  
KW malignant tumor; hypertension; hypotension; obesity; bulimia; anorexia;  
KW asthma; manic depression; dementia; delirium; mental retardation;  
KW Huntington's disease; Tourette's syndrome; schizophrenia;  
KW mental disorder; sexual development disorder; blood cascade dysfunction;  
KW stroke; growth disorder.  
XX OS Homo sapiens.  
XX PN WO200222802-A1.  
XX PD 21-MAR-2002.  
XX PF 13-SEP-2001; 2001WO-US28462.  
XX PR 13-SEP-2000; 2000US-232455P.  
XX PR 13-SEP-2000; 2000US-232463P.  
XX PR 02-OCT-2000; 2000US-237293P.  
XX PR 07-NOV-2000; 2000US-246269P.  
XX PR 20-NOV-2000; 2000US-252049P.

XX PA (SMIK) SMITHKLINE BEECHAM CORP.  
XX PA (SMIK) SMITHKLINE BEECHAM PLC.  
XX PA (GLAX) GLAXO GROUP LTD.  
XX PI Agarwal P, Gogswell JP, Lai Y, Martensen SA, Smith RF, Strum JC;  
PI Xie Q;  
XX DR WPI: 2002-393963/42.  
XX N-PSDB: ABL57743.

XX PT Novel isolated secreted polypeptides and polynucleotides encoding them  
XX useful for treating cancer, Alzheimer's disease, tumor metastasis,  
XX PT autosomal recessive atypical hemolytic uremic syndrome, wound healing  
XX disorder -  
XX PS 1; Page235-237; 246pp; English.  
XX CC The invention relates to a novel isolated polypeptide (ABB80569-ABB80612)  
XX (secreted polypeptide) which is encoded by any one of 44 polynucleotide  
XX sequences (ABL57705-ABL57748) given in the specification. The  
XX polypeptides have immunosuppressive, cytostatic, nootropic,  
XX neuroprotective, antitumor, vulnery, antineoplastic, ophthalmological,  
XX antiparkinsonian, antirheumatic, antidiabetic, dermatological,  
XX hypotensive, cerebroprotective, virucide, and antineoplastic activity.  
XX The polynucleotide and polypeptide are useful for treating diabetes,  
XX malignant tumours, hyper- and hypotension, obesity, bulimia, anorexia,  
XX asthma, manic depression, dementia, delirium, mental retardation,  
XX Huntington's disease, Tourette's syndrome, schizophrenia, growth, mental  
XX or sexual development disorders, and dysfunctions of the blood cascade  
XX system including those leading to stroke.  
XX SQ Sequence 904 AA;

Query Match 57.1%; Score 40; DB 23; Length 904;  
Best Local Similarity 75.0%; Pred. NO. 4.2e+02;  
Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SNPEVKLPLP 12



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DB      435 SPPVEDLPPKS 446
      1 ||||| ||| |
RESULT 15
AAU86840
ID      AAU86840 standard; Protein; 48 AA.
XX
XX      AAU86840;
AC
XX
DT      21-MAY-2002 (first entry)
XX
DE      Novel human connective tissue related polypeptide #406.
XX
KW      Human; connective tissue related disorder; cancer; cytoslatic.
XX
OS      Homo sapiens.
XX      WO200155343-A1.
XX
PD      02-AUG-2001.
XX
PF      17-JAN-2001; 2001WO-US01322.
XX
PR      31-JAN-2000; 2000US-0179065.
PR      04-FEB-2000; 2000US-0180628.
PR      24-FEB-2000; 2000US-0184664.
PR      02-MAR-2000; 2000US-0186350.
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PR      17-MAR-2000; 2000US-0190076.
PR      18-MAR-2000; 2000US-0198123.
PR      19-MAY-2000; 2000US-0205515.
PR      07-JUN-2000; 2000US-0209467.
PR      28-JUN-2000; 2000US-0214886.
PR      30-JUN-2000; 2000US-0215135.
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PR      26-JUL-2000; 2000US-0220963.
PR      26-JUL-2000; 2000US-0220964.
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PR      14-AUG-2000; 2000US-0225759.
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PR      22-AUG-2000; 2000US-0226881.
PR      22-AUG-2000; 2000US-0226881.
PR      22-AUG-2000; 2000US-0226868.
PR      23-AUG-2000; 2000US-0227182.
PR      30-AUG-2000; 2000US-0227029.
PR      30-AUG-2000; 2000US-0228924.
PR      01-SEP-2000; 2000US-0228287.
PR      01-SEP-2000; 2000US-0228343.
PR      01-SEP-2000; 2000US-0229344.
PR      01-SEP-2000; 2000US-0229345.
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PR      05-SEP-2000; 2000US-0229513.
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PR      08-SEP-2000; 2000US-0231414.
PR      08-SEP-2000; 2000US-0232080.
PR      08-SEP-2000; 2000US-0232081.
PR      12-SEP-2000; 2000US-0231968.
PR      14-SEP-2000; 2000US-0232397.
PR      14-SEP-2000; 2000US-0232398.
PR      14-SEP-2000; 2000US-0232399.
PR      14-SEP-2000; 2000US-0232400.
PR      14-SEP-2000; 2000US-0232401.
PR      14-SEP-2000; 2000US-0233063.
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PR      14-SEP-2000; 2000US-0233065.
PR      21-SEP-2000; 2000US-0234223.
PR      21-SEP-2000; 2000US-0234274.
PR      25-SEP-2000; 2000US-0234997.
PR      25-SEP-2000; 2000US-0234998.
PR      26-SEP-2000; 2000US-0235484.
PR      27-SEP-2000; 2000US-0235834.
PR      27-SEP-2000; 2000US-0235836.
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PR      29-SEP-2000; 2000US-0236369.
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PR      02-OCT-2000; 2000US-0236802.
PR      02-OCT-2000; 2000US-0237037.
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PR      13-OCT-2000; 2000US-0239935.
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PR      20-OCT-2000; 2000US-0240960.
PR      20-OCT-2000; 2000US-0241221.
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PR      20-OCT-2000; 2000US-0241787.
PR      20-OCT-2000; 2000US-0241808.
PR      20-OCT-2000; 2000US-0241809.
PR      20-OCT-2000; 2000US-0241826.
PR      01-NOV-2000; 2000US-0244617.
PR      08-NOV-2000; 2000US-0246474.
PR      08-NOV-2000; 2000US-0246475.
PR      08-NOV-2000; 2000US-0246476.
PR      08-NOV-2000; 2000US-0246477.
PR      08-NOV-2000; 2000US-0246478.
PR      08-NOV-2000; 2000US-0246523.
PR      08-NOV-2000; 2000US-0246524.
PR      08-NOV-2000; 2000US-0246525.
PR      08-NOV-2000; 2000US-0246526.
PR      08-NOV-2000; 2000US-0246527.
PR      08-NOV-2000; 2000US-0246528.
PR      08-NOV-2000; 2000US-0246532.
PR      08-NOV-2000; 2000US-0246609.
PR      08-NOV-2000; 2000US-0246610.
PR      08-NOV-2000; 2000US-0246611.
PR      08-NOV-2000; 2000US-0246613.
PR      17-NOV-2000; 2000US-0246207.
PR      17-NOV-2000; 2000US-0246208.
PR      17-NOV-2000; 2000US-0249209.
PR      17-NOV-2000; 2000US-0249210.
PR      17-NOV-2000; 2000US-0249211.
PR      17-NOV-2000; 2000US-0249212.
PR      17-NOV-2000; 2000US-0249213.
PR      17-NOV-2000; 2000US-0249214.
PR      17-NOV-2000; 2000US-0249215.
PR      17-NOV-2000; 2000US-0249216.
PR      17-NOV-2000; 2000US-0249217.
PR      17-NOV-2000; 2000US-0249218.
PR      17-NOV-2000; 2000US-0249244.
PR      17-NOV-2000; 2000US-0249245.
PR      17-NOV-2000; 2000US-0249264.
PR      17-NOV-2000; 2000US-0249265.
PR      17-NOV-2000; 2000US-0249297.
PR      17-NOV-2000; 2000US-0249299.
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PR 17-NOV-2000; 2000US-0249300.  
 PR 01-DEC-2000; 2000US-0250160.  
 PR 01-DEC-2000; 2000US-0250391.  
 PR 05-DEC-2000; 2000US-0251030.  
 PR 05-DEC-2000; 2000US-0251988.  
 PR 05-DEC-2000; 2000US-0256719.  
 PR 06-DEC-2000; 2000US-0251479.  
 PR 08-DEC-2000; 2000US-0251856.  
 PR 08-DEC-2000; 2000US-0251868.  
 PR 08-DEC-2000; 2000US-0251869.  
 PR 08-DEC-2000; 2000US-0251989.  
 PR 11-DEC-2000; 2000US-0254097.  
 PR 05-JAN-2001; 2001US-0259678.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Barash SC, Ruben SM;  
 XX  
 DR WPI; 2001-565190/63.  
 N-PSDB; ABK42018.  
 XX  
 PT Nucleic acid encoding novel connective tissue associated polypeptides,  
 PT used in diagnosing, preventing, treating or ameliorating a disorder  
 PT such as cancer or rheumatoid arthritis -  
 XX  
 PS Claim 11; SEQ ID No 905; 673pp; English.  
 XX  
 CC The present invention relates to the isolation of novel human  
 CC connective tissue related polypeptides and the polynucleotide  
 CC (CDNA and genomic) sequences encoding them. The sequences of the  
 CC invention are useful in the diagnosis, treatment, prevention and/or  
 CC prognosis of diseases associated with connective tissue(s), including  
 CC cancer. The polynucleotide sequences of the invention are also useful  
 CC in gene therapy. AU86435-AU86923 represent the novel human connective  
 CC tissue related polypeptides.  
 CC Note: The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 SQ Sequence 48 AA;  
 Query Match 55.7%; Score 39; DB 22; Length 48;  
 Best Local Similarity 80.0%; Pred. No. 24;  
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Caps 0;  
 OY 4 PVEKLPLSL 13  
 |:| | | | | | |  
 DB 33 PLETLPLSL 42

Search completed: January 12, 2003, 04:15:03  
 Job time : 75 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2003, 04:14:30 ; Search time 23 Seconds  
(without alignments)  
17,910 Million cell updates/sec

Title: HANDENTERED  
Perfect score: 70  
Sequence: 1 snpveklplslk 14

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
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5: /cgn2\_6/ptodata/1/1aa/PCRTUS.COMB.pep:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	39	55.7	653	1	US-08-339-152A-16
2	39	55.7	653	2	US-08-007-999B-3
3	39	55.7	653	3	US-08-689-276A-3
4	37	52.9	305	1	US-08-680-726A-80
5	37	52.9	305	4	US-09-092-409-80
6	37	52.9	724	2	US-08-562-737-25
7	36.5	52.1	687	2	US-08-540-804-4
8	36.5	52.1	687	2	US-08-218-265-4
9	36.5	52.1	687	2	US-08-521-872-4
10	36.5	52.1	687	4	US-08-590-399-4
11	36	51.4	104	4	US-08-936-165A-368
12	36	51.4	315	4	US-09-362-318-2
13	36	51.4	464	1	US-07-688-352C-16
14	36	51.4	464	2	US-08-474-379C-16
15	36	51.4	464	2	US-09-146-249A-16
16	36	51.4	464	3	US-08-206-188B-16
17	36	51.4	464	5	PCR-US91-02714-16
18	36	51.4	528	2	US-08-466-589-2
19	36	51.4	528	2	US-08-700-636-2
20	36	51.4	528	3	US-08-467-574-2
21	36	51.4	528	4	US-09-217-345-2
22	36	51.4	529	4	US-08-496-855A-2
23	36	51.4	529	4	US-08-487-596-2
24	36	51.4	600	4	US-09-423-468A-13
25	35	50.0	17	2	US-08-964-725-15
26	35	50.0	93	2	US-08-964-725-14
27	35	50.0	388	2	US-08-282-197C-56

28	35	50.0	1263	4	US-09-446-504-6	Sequence 6, Appl
29	35	50.0	1263	4	US-09-712-266-6	Sequence 6, Appl
30	35	50.0	1263	4	US-09-091-889A-4	Sequence 4, Appl
31	35	50.0	1727	2	US-08-477-451-10	Sequence 10, Appl
32	34	48.6	237	4	US-08-999-774A-8	Sequence 8, Appl
33	34	48.6	258	4	US-08-914-999-16	Sequence 16, Appl
34	34	48.6	266	4	US-08-904-234-3	Sequence 3, Appl
35	34	48.6	429	2	US-08-677-049-5	Sequence 5, Appl
36	34	48.6	463	3	US-09-082-310-1	Sequence 1, Appl
37	34	48.6	463	3	US-09-575-205-1	Sequence 5071, Ap
38	34	48.6	507	4	US-09-134-001C-5071	Sequence 32, Appl
39	34	48.6	532	1	US-08-339-152A-32	Sequence 2, Appl
40	34	48.6	548	3	US-08-942-001-2	Sequence 2, Appl
41	34	48.6	548	4	US-09-337-386-2	Sequence 2, Appl
42	34	48.6	548	4	US-09-846-922-2	Sequence 2, Appl
43	34	48.6	575	4	US-08-924-345-3	Sequence 3, Appl
44	34	48.6	640	4	US-09-177-165A-30	Sequence 30, Appl
45	34	48.6	807	4	US-09-177-650-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1

US-08-339-152A-16  
Sequence 16, Application US/08339152A  
Patent No. 5643726

GENERAL INFORMATION:  
APPLICANT: Tanzl, Rudolph E.

APPLICANT: Kovacs, Dora M.

TITLE OF INVENTION: Methods For Modulating Transcription

TITLE OF INVENTION: From the Amyloid -Protein Precursor (APP) Promoter

NUMBER OF SEQUENCES: 33

CORRESPONDENCE ADDRESS:

ADDRESS: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.

STREET: 1100 New York Ave., NW, Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/339,152A

FILING DATE: 10-NOV-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Steffe, Eric K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 0609.4120000

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2540

TELEX:

INFORMATION FOR SEQ. ID NO. 16:

SEQUENCE CHARACTERISTICS:

LENGTH: 653 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-339-152A-16

Query Match

Best Local Similarity

Matches 8; Conservative

3 PPKVKKLPLSL 13

11: |||||

Db 17 PPKVKKLPLSL 27

Score 39; DB 1; Length 653;

Pred. No. 77;

Mismatches 2; Indels 0; Gaps 0;

RESULT 2  
US-08-007-999B-3  
; Sequence 3, Application US/08007999B  
; Patent No. 5851787  
; GENERAL INFORMATION:  
; APPLICANT: Masco, Wilma  
; APPLICANT: Bupp, Keith  
; APPLICANT: Magendantz, Margaret  
; APPLICANT: Tanzl, Rudolph  
; APPLICANT: Solomon, Frank  
; TITLE OF INVENTION: AMYLOID PRECURSOR-LIKE PROTEIN AND USES  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
; STREET: 1100 New York Ave., NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/007,999B  
; FILING DATE: 21-JAN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/872,642  
; FILING DATE: 20-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/930,022  
; FILING DATE: 17-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Townsend, G. Kevin  
; REGISTRATION NUMBER: 34,033  
; REFERENCE/DOCKET NUMBER: 0609.3520002/JAG/GKT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)371-2571  
; TELEFAX: (202)371-2540  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 653 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-007-999B-3

Query Match 55.7%; Score 39; DB 2; Length 653;  
Best Local Similarity 72.7%; Pred. No. 77;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PVEKLLPLSL 13  
||: |||||  
Db 17 PPLPLPLSL 27

RESULT 3  
US-08-689-276A-3  
; Sequence 3, Application US/08689276A  
; Patent No. 5891991  
; GENERAL INFORMATION:  
; APPLICANT: Masco, Wilma  
; APPLICANT: Bupp, Keith  
; APPLICANT: Magendantz, Margaret  
; APPLICANT: Tanzl, Rudolph  
; APPLICANT: Solomon, Frank  
; TITLE OF INVENTION: AMYLOID PRECURSOR-LIKE PROTEIN AND USES  
; NUMBER OF SEQUENCES: 19  
; CORRESPONDENCE ADDRESSES:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.  
; STREET: 1100 New York Ave., NW  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20005  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/689,276A  
; FILING DATE: 06-AUG-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/007,999  
; FILING DATE: 21-JAN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/872,642  
; FILING DATE: 20-APR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/930,022  
; FILING DATE: 17-AUG-1992  
; ATTORNEY/AGENT INFORMATION:  
; NAME: JORGE A. GOLDSTEIN  
; REGISTRATION NUMBER: 29,021  
; REFERENCE/DOCKET NUMBER: 0609.3520003  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)371-2571  
; TELEFAX: (202)371-2540  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 653 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-689-276A-3

Query Match 55.7%; Score 39; DB 2; Length 653;  
Best Local Similarity 72.7%; Pred. No. 77;  
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PVEKLLPLSL 13  
||: |||||  
Db 17 PPLPLPLSL 27

RESULT 4  
US-08-680-726A-80  
; Sequence 80, Application US/08680726A  
; Patent No. 5804197  
; GENERAL INFORMATION:  
; APPLICANT: Haanes, Elizabeth J.  
; APPLICANT: Frank, Rexann S.  
; TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUS  
; NUMBER OF SEQUENCES: 92  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Sheridan Ross & McIntosh  
; STREET: 1700 Lincoln Street, Suite 3500  
; CITY: Denver  
; STATE: Colorado  
; COUNTRY: U.S.A.  
; ZIP: 80203  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/680,726A  
; FILING DATE: 12-JUL-1996  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:

NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2618-46-C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 305 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-680-726A-80

Query Match  
Best Local Similarity 52.9%; Score 37; DB 1; Length 305;  
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 NPPEVKLPLSLK 14  
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Db 107 HPTVEKLNIPYDLK 119

RESULT 5  
US-09-092-409-80  
Sequence 80, Application US/09092409  
Patent No. 6159478  
GENERAL INFORMATION:  
APPLICANT: Haanes, Elizabeth J.  
APPLICANT: Frank, Rexann S.  
TITLE OF INVENTION: RECOMBINANT CANINE HERPESVIRUSES  
NUMBER OF SEQUENCES: 92  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheridan Ross & McIntosh  
STREET: 1700 Lincoln Street, Suite 3500  
CITY: Denver  
STATE: Colorado  
COUNTRY: U.S.A.  
ZIP: 80203  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/092,409  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/680,726  
FILING DATE: 12-JUL-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Connell, Gary J.  
REGISTRATION NUMBER: 32,020  
REFERENCE/DOCKET NUMBER: 2618-46-C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (303) 863-9700  
TELEFAX: (303) 863-0223  
INFORMATION FOR SEQ ID NO: 80:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 305 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-092-409-80

Query Match  
Best Local Similarity 52.9%; Score 37; DB 4; Length 305;  
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 NPPEVKLPLSLK 14  
: | | | | | | |  
Db 107 HPTVEKLNIPYDLK 119

RESULT 6  
US-09-562-737-25  
Sequence 25, Application US/09562737  
Patent No. 6428667  
GENERAL INFORMATION:  
APPLICANT: Herz, Joachim  
APPLICANT: Gotthardt, Michael  
TITLE OF INVENTION: LDL Receptor Signaling Pathways  
FILE REFERENCE: UTSW0708  
CURRENT APPLICATION NUMBER: US/09/562,737  
CURRENT FILING DATE: 2000-05-01  
NUMBER OF SEQ ID NOS: 132  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 25  
LENGTH: 724  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-562-737-25

Query Match  
Best Local Similarity 52.9%; Score 37; DB 4; Length 724;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 PYVEKLIPLSL 13  
: | | | | | | |  
Db 153 PYVEKLIPLSL 163

RESULT 7  
US-08-540-804-4  
Sequence 4, Application US/08540804  
Patent No. 5919666  
GENERAL INFORMATION:  
APPLICANT: Young, Richard A.  
APPLICANT: Koleske, Anthony J.  
APPLICANT: Thompson, Craig M.  
APPLICANT: Chao, David M.  
TITLE OF INVENTION: No. 5919666el Factors which Modify Gene  
TITLE OF INVENTION: Transcription and Methods of Use Therefor  
NUMBER OF SEQUENCES: 39  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.  
STREET: Two Militia Drive  
CITY: Lexington  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02173  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/540,804  
FILING DATE: 11-OCT-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/521,872  
FILING DATE: 21-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/218,265  
FILING DATE: 25-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: WH194-03A2  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240



OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/590,399  
FILING DATE: 26-JAN-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/540,804  
FILING DATE: 11-OCT-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/521,872  
FILING DATE: 31-AUG-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/218,265  
FILING DATE: 25-MAR-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Granahan, Patricia  
REGISTRATION NUMBER: 32,227  
REFERENCE/DOCKET NUMBER: WH194-03A3  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-861-6240  
TELEFAX: 617-861-9540  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 687 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-590-399-4

Query Match 52.1%; Score 36.5; DB 4; Length 687;  
Best Local Similarity 38.1%; Pred. No. 2.2e+02;  
Matches 8; Conservative 5; Mismatches 1; Indels 7; Gaps 1;

OY 1 SNP-----PVEKLPISLK 14  
||| |::|:|:|:|:  
Db 88 SNPEITGSMPLDPLIPILIR 108

RESULT 11  
US-08-936-165A-368  
Sequence 368, Application US/08936165A  
Patent No. 6348582  
GENERAL INFORMATION:  
APPLICANT: Black, Michael  
APPLICANT: Burnham, Martin  
APPLICANT: Hodgson, John  
APPLICANT: Knowles, David  
APPLICANT: Lonetto, Michael  
APPLICANT: Nicholas, Richard  
APPLICANT: Pratt, Julie  
APPLICANT: Reichard, Richard  
APPLICANT: Rosenberg, Martin  
APPLICANT: Ward, Judith  
TITLE OF INVENTION: Pol. 6348582el Prokaryotic Polynucleotides,  
TITLE OF INVENTION: Polypeptides and Their Uses  
NUMBER OF SEQUENCES: 534  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Smithkline Beecham Corporation  
STREET: 709 Swedeland Road  
CITY: King of Prussia  
STATE: PA  
COUNTRY: USA  
ZIP: 19406-0939  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/936,165A  
FILING DATE: 24-SEP-1997  
CLASSIFICATION: 536

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/027,032  
FILING DATE: 24-SEP-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Gimmli, Edward R  
REGISTRATION NUMBER: 38,891  
REFERENCE/DOCKET NUMBER: P50549  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 610-270-4478  
TELEFAX: 610-270-5090  
TELEX:  
INFORMATION FOR SEQ ID NO: 368:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 104 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: Protein  
US-08-936-165A-368

Query Match 51.4%; Score 36; DB 4; Length 104;  
Best Local Similarity 60.0%; Pred. No. 32;  
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 SNPEVKLP 10  
|||:|:  
Db 17 SNPEILPLIP 26

RESULT 12  
US-09-362-318-2  
Sequence 2, Application US/09362318  
Patent No. 6077993  
GENERAL INFORMATION:  
APPLICANT: Mahajan, Pramod B.  
TITLE OF INVENTION: Maize Repair Protein Orthologue-1 and  
FILE REFERENCE: 0934  
CURRENT APPLICATION NUMBER: US/09/362,318  
CURRENT FILING DATE: 1999-07-27  
EARLIER APPLICATION NUMBER: 60/099,280  
EARLIER FILING DATE: 1998-09-03  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 2  
LENGTH: 315  
TYPE: PRT  
ORGANISM: Zea mays  
US-09-362-318-2

Query Match 51.4%; Score 36; DB 3; Length 315;  
Best Local Similarity 66.7%; Pred. No. 1.1e+02;  
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 NPPEVKLP 10  
||:|:|:  
Db 72 NPALEKLP 80

RESULT 13  
US-07-688-352C-16  
Sequence 16, Application US/07688352C  
Patent No. 5527896  
GENERAL INFORMATION:  
APPLICANT: Wiegler, Michael H.  
APPLICANT: Colicelli, John J.  
TITLE OF INVENTION: Cloning by Complementation and Related  
TITLE OF INVENTION: Processes  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark

STREET: Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/688,352C  
FILING DATE: 19910419  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/511,715  
FILING DATE: 20-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Borun, Michael F.  
REGISTRATION NUMBER: 25447  
REFERENCE/DOCKET NUMBER: 27805/30197  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 464 amino acids  
TYPE: AMINO ACID  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-07-688-352C-16

Query Match 51.4%; Score 36; DB 1; Length 464;  
Best Local Similarity 55.6%; Pred. No. 1.7e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPVEKLLP 10  
Db 144 DPPIESLP 152

RESULT 14  
US-08-474-379C-16  
Sequence 16, Application US/08474379C  
Patent No. 5977305  
GENERAL INFORMATION:  
APPLICANT: Migler, Michael H.  
APPLICANT: Colicelli, John J.  
TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED  
TITLE OF INVENTION: PROCESSES  
NUMBER OF SEQUENCES: 88  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive/6300 Sears Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/474,379C  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/511,715  
FILING DATE: 20-APR-1990  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/206,188

FILING DATE: 01-MAR-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/688,352  
FILING DATE: 19-APR-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Clough, David W.  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 27866/32771  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 464 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-474-379C-16

Query Match 51.4%; Score 36; DB 2; Length 464;  
Best Local Similarity 55.6%; Pred. No. 1.7e+02;  
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 NPVEKLLP 10  
Db 144 DPPIESLP 152

RESULT 15  
US-09-146-249A-16  
Sequence 16, Application US/09146249A  
Patent No. 6069240  
GENERAL INFORMATION:  
APPLICANT: Migler, Michael H.  
APPLICANT: Colicelli, John J.  
TITLE OF INVENTION: Cloning by Complementation and Related  
TITLE OF INVENTION: Processes  
NUMBER OF SEQUENCES: 85  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 6300 Sears Tower, 233 South Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States of America  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/146,249A  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/511,715  
FILING DATE: 20-APR-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Clough, David W.  
REGISTRATION NUMBER: 36,107  
REFERENCE/DOCKET NUMBER: 27866/32771  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 312/474-6300  
TELEFAX: 312/474-0448  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 464 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-146-249A-16

Query Match 51.4%; Score 36; DB 3; Length 464;



Best Local Similarity 55.6%; Pred. NO. 1.7e+02;  
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Oy 2 NPPVERLIP 10  
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Db 144 DPPIESLIP 152

Search completed: January 12, 2003, 04:18:44  
Job time : 26 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 12, 2003, 04:15:10 ; Search time 17 Seconds  
(without alignments)  
15.977 Million cell updates/sec

Title: HANDENTERED  
Perfect score: 70  
Sequence: 1 snpyekllpislk 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 118974 seqs, 19401057 residues  
Total number of hits satisfying chosen parameters: 118974

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubppaa/US08\_NEW\_PUB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubppaa/PCY\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubppaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubppaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubppaa/US07\_NEW\_PUB.pep.\*
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- 10: /cgn2\_6/ptodata/1/pubppaa/US09\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubppaa/US10\_NEW\_PUB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubppaa/US10\_PUBCOMB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubppaa/US60\_NEW\_PUB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubppaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	39	55.7	48	10	US-09-764-847-905
2	38	54.3	221	10	US-09-925-299-967
3	38	54.3	282	10	US-09-815-242-5576
4	38	54.3	292	10	US-09-815-242-12440
5	37	52.9	283	10	US-09-815-242-10199
6	37	52.9	467	10	US-09-804-551B-10
7	36	51.4	104	10	US-09-939-980-368
8	36	51.4	188	10	US-09-734-569-134
9	36	51.4	203	10	US-09-810-997-4
10	36	51.4	291	10	US-09-815-242-11818
11	36	51.4	303	10	US-09-864-761-34235
12	36	51.4	324	10	US-09-746-801A-61
13	36	51.4	333	10	US-09-815-242-11871
14	36	51.4	401	10	US-09-815-242-5506
15	36	51.4	401	10	US-09-815-242-12261
16	36	51.4	528	10	US-09-892-985-2
17	36	51.4	551	10	US-09-815-242-10500
18	35	50.0	93	9	US-10-081-617-32
19	35	50.0	93	12	US-10-052-586-244

20	35	50.0	270	10	US-09-911-826A-8	Sequence 8, Appli
21	35	50.0	513	9	US-09-738-626-3645	Sequence 3645, Ap
22	35	50.0	550	10	US-09-934-323-6	Sequence 6, Appli
23	35	50.0	603	9	US-09-764-868-705	Sequence 705, App
24	35	50.0	649	9	US-09-984-245-197	Sequence 197, App
25	35	50.0	783	10	US-09-825-144-2	Sequence 2, Appli
26	35	50.0	829	10	US-09-825-144-4	Sequence 4, Appli
27	35	50.0	835	10	US-09-934-323-2	Sequence 2, Appli
28	35	50.0	836	10	US-09-934-323-5	Sequence 5, Appli
29	35	50.0	1263	10	US-09-971-309-6	Sequence 6, Appli
30	34	48.6	69	10	US-09-864-761-42307	Sequence 42307, A
31	34	48.6	123	10	US-09-764-847-509	Sequence 509, App
32	34	48.6	258	10	US-09-994-485-16	Sequence 16, Appli
33	34	48.6	259	9	US-09-832-292-3	Sequence 3, Appli
34	34	48.6	294	9	US-09-738-626-6177	Sequence 6177, Ap
35	34	48.6	328	10	US-09-864-761-35526	Sequence 35526, A
36	34	48.6	463	9	US-10-155-613-1	Sequence 1, Appli
37	34	48.6	479	10	US-09-881-752A-312	Sequence 312, App
38	34	48.6	538	10	US-09-815-242-11125	Sequence 11125, A
39	34	48.6	640	9	US-10-060-019-30	Sequence 30, Appli
40	34	48.6	1146	9	US-09-832-292-10	Sequence 10, Appli
41	34	48.6	1146	10	US-09-824-734-2	Sequence 2, Appli
42	34	48.6	1146	10	US-09-994-485-6	Sequence 6, Appli
43	33	47.1	57	10	US-09-864-761-43961	Sequence 43961, A
44	33	47.1	142	10	US-09-764-847-975	Sequence 975, App
45	33	47.1	149	10	US-09-864-761-43311	Sequence 43311, A

## ALIGNMENTS

RESULT 1  
US-09-764-847-905  
Sequence 905, Application US/09764847  
Patent No. US20020132767A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
FILE REFERENCE: PC009  
CURRENT APPLICATION NUMBER: US/09/764,847  
CURRENT FILING DATE: 2001-01-17  
Prior application data removed - consult PAM or file wrapper  
NUMBER OF SEQ ID NOS: 2003  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 905  
LENGTH: 48  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (30)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
NAME/KEY: SITE  
LOCATION: (44)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-764-847-905

Query Match 55.7% Score 39; DB 10; Length 48;  
Best Local Similarity 80.0% Pred. No. 2.7;  
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 PVEKILPLSL 13  
Db 33 PLERLPLSL 42

RESULT 2  
US-09-925-299-967  
Sequence 967, Application US/09925299  
Patent No. US20020055627A1  
GENERAL INFORMATION:  
APPLICANT: Rosen et al.  
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

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FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 967
LENGTH: 221
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-299-967
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Query Match 54.3% Score 38; DB 10; Length 221;
Best Local Similarity 61.5%; Pred. No. 23;
Matches 8; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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QY 1 NNPVEKLPLSL 13
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Db 7 SRPPLTPSLPLSL 19
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RESULT 3
US-09-815-242-5576
Sequence 5576, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5576
LENGTH: 282
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-5576
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Query Match 54.3% Score 38; DB 10; Length 282;
Best Local Similarity 80.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 2 NNPVEKLPL 11
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Db 71 NNPVEKLPL 80
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RESULT 4
US-09-815-242-12440
Sequence 12440, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
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```
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12440
LENGTH: 292
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12440
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Query Match 54.3% Score 38; DB 10; Length 292;
Best Local Similarity 80.0%; Pred. No. 32;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 2 NNPVEKLPL 11
    | | | | |
Db 77 NNPVEKLPL 86
```

```
RESULT 5
US-09-815-242-10199
Sequence 10199, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
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; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10199
; LENGTH: 283
; TYPE: PRT
; ORGANISM: Escherichia coli
;
US-09-815-242-10199

Query Match
Best Local Similarity 52.9%; Score 37; DB 10; Length 283;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 NPPEVKLPL 11
DB 73 NHPITLPL 82

RESULT 6
US-09-804-551B-10
; Sequence 10, Application US/09804551B
; Patent No. US20020056151A1
; GENERAL INFORMATION:
; APPLICANT: Bayer Aktiengesellschaft
; TITLE OF INVENTION: Receptors for peptides from insects
; FILE REFERENCE: Le A 34 394
; CURRENT APPLICATION NUMBER: US/09/804,551B
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: DE 100 13 618.4
; PRIOR FILING DATE: 2000-03-18
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 467
; TYPE: PRT
; ORGANISM: Drosophila melanogaster
;
US-09-804-551B-10

Query Match
Best Local Similarity 52.9%; Score 37; DB 10; Length 467;
Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 SNPEVKLPL 12
DB 388 SNPIPLPL 399

RESULT 7
US-09-939-980-368
; Sequence 368, Application US/09939980
; Patent No. US20020082234A1
; GENERAL INFORMATION:
; APPLICANT: Black, Michael
; Burnham, Martin
; Hodgson, John
; Knowles, David
; Lonetto, Michael
; Nicholas, Richard
; Pratt, Julie
; Reichard, Richard
; Rosenberg, Martin
; Ward, Judith
;
TITLE OF INVENTION: No. US20020082234A1el Prokaryotic Polynucleotides,
Polypeptides and Their Uses
NUMBER OF SEQUENCES: 534
CORRESPONDENCE ADDRESS:
```

```

; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
;
COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
;
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/939,980
; FILING DATE: 27-Aug-2001
; CLASSIFICATION: <Unknown>
;
PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/936,165
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimmil, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P50549
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX: <Unknown>
;
INFORMATION FOR SEQ ID NO: 368:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 104 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Protein
;
US-09-939-980-368

Query Match
Best Local Similarity 51.4%; Score 36; DB 10; Length 104;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 SNPEVKLPL 10
DB 17 SNPIPLPL 26

RESULT 8
US-09-734-569-134
; Sequence 134, Application US/09734569
; Patent No. US20020064816A1
; GENERAL INFORMATION:
; APPLICANT: Lerchl, Jens
; APPLICANT: Renz, Andreas
; APPLICANT: Ehrhardt, Thomas
; APPLICANT: Reinold, Andreas
; APPLICANT: Clippus, Petra
; APPLICANT: Bischoff, Friedrich
; APPLICANT: Frank, Markus
; APPLICANT: Freund, Annette
; APPLICANT: Duwenig, Elke
; APPLICANT: Schmidt, Ralf-Michael
; APPLICANT: Reski, Ralf
;
TITLE OF INVENTION: Moss genes from Physcomitrella patens encoding proteins involv
FILE REFERENCE: BASF-NAE-1332-99-US
; CURRENT APPLICATION NUMBER: US/09/734,569
; CURRENT FILING DATE: 2001-05-24
; PRIOR APPLICATION NUMBER: US 60/171,101
; PRIOR FILING DATE: 1999-12-16
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn Ver. 2.1/WordPerfect 6.1
; SEQ ID NO 134
; LENGTH: 188
; TYPE: PRT
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ORGANISM: Physcomitrella patens  
US-09-734-569-134

Query Match  
Best Local Similarity 51.4%; Score 36; DB 10; Length 188;  
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 NPVEKLLP 10  
| | | | |  
Db 9 NYPVDKLLP 17

RESULT 9

US-09-810-997-4  
; Sequence 4, Application US/09810997  
; Patent No. US20020007501A1  
; GENERAL INFORMATION:  
; APPLICANT: Song, Xiaoling  
; APPLICANT: Fan, Hao  
; APPLICANT: Wei, Zhong-Min  
; TITLE OF INVENTION: RECEPTORS FOR HYPERSENSITIVE RESPONSE ELICITORS AND  
; TITLE OF INVENTION: USES THEREOF  
; FILE REFERENCE: 21829/62  
; CURRENT APPLICATION NUMBER: US/09/810,997  
; CURRENT FILING DATE: 2001-03-16  
; PRIOR APPLICATION NUMBER: 60/191,649  
; PRIOR FILING DATE: 2000-03-23  
; PRIOR APPLICATION NUMBER: 60/250,710  
; PRIOR FILING DATE: 2000-12-01  
; NUMBER OF SEQ ID NOS: 9  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 203  
; TYPE: PRT  
; ORGANISM: Oryza  
US-09-810-997-4

Query Match  
Best Local Similarity 51.4%; Score 36; DB 10; Length 203;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PVEKLLPLSL 13  
| | | | |  
Db 78 PPTGRLPLTL 88

RESULT 10

US-09-815-242-11818  
; Sequence 11818, Application US/09815242  
; Patent No. US20020061569A1  
; GENERAL INFORMATION:  
; APPLICANT: Haselbeck, Robert  
; APPLICANT: Ohlisen, Karl L.  
; APPLICANT: Zyskind, Judith W.  
; APPLICANT: Wall, Daniel  
; APPLICANT: Treweek, John D.  
; APPLICANT: Carr, Grant J.  
; APPLICANT: Yamamoto, Robert T.  
; APPLICANT: Xu, H. Howard  
; TITLE OF INVENTION: Identification of Essential Genes in  
; TITLE OF INVENTION: Prokaryotes  
; FILE REFERENCE: ELITRA.011A  
; CURRENT APPLICATION NUMBER: US/09/815,242  
; CURRENT FILING DATE: 2001-03-21  
; PRIOR APPLICATION NUMBER: 60/191,078  
; PRIOR FILING DATE: 2000-03-21  
; PRIOR APPLICATION NUMBER: 60/206,848  
; PRIOR FILING DATE: 2000-05-23  
; PRIOR APPLICATION NUMBER: 60/207,727  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: 60/242,578  
; PRIOR FILING DATE: 2000-10-23  
; PRIOR APPLICATION NUMBER: 60/253,625

; PRIOR FILING DATE: 2000-11-27  
; PRIOR APPLICATION NUMBER: 60/257,931  
; PRIOR FILING DATE: 2000-12-22  
; PRIOR APPLICATION NUMBER: 60/269,308  
; PRIOR FILING DATE: 2001-02-16  
; NUMBER OF SEQ ID NOS: 1410  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 11818  
; LENGTH: 291  
; TYPE: PRT  
; ORGANISM: Pseudomonas aeruginosa  
US-09-815-242-11818

Query Match  
Best Local Similarity 51.4%; Score 36; DB 10; Length 291;  
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 2 NPVEKLLPL 11  
| | | | |  
Db 75 NHPVEMLPLM 84

RESULT 11

US-09-864-761-34235  
; Sequence 34235, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wensheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY  
; FILE REFERENCE: Aegm1ca-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117

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; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 34235
; LENGTH: 303
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL049538.8
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 8.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 9.7
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 9.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 8.7
; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 7
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 6.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 10
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 13
; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 6.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 8.4
; OTHER INFORMATION: SWISSPROT HIT: P97680, EVALUATE 2.00e-03
; US-09-864-761-34235

```

```

Query Match
Best Local Similarity 51.4%; Score 36; DB 10; Length 303;
Pred. No. 72;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 2 NPPEKLLP 10
DB 291 DPPEKLLP 299

```

```

RESULT 12
US-09-746-801A-61
; Sequence 61, Application US/09746801A
; Patent No. US20020083494A1
; GENERAL INFORMATION:
; APPLICANT: Wagner, et al.
; TITLE OF INVENTION: GENES REGULATING CIRCADIAN CLOCK FUNCTION AND PHOTOPERIODISM
; FILE REFERENCE: 1505-34357
; CURRENT APPLICATION NUMBER: US/09/746,801A
; CURRENT FILING DATE: 2000-12-20
; NUMBER OF SEQ ID NOS: 68
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 61
; LENGTH: 324
; TYPE: PRT
; ORGANISM: Brassica sp.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (188)..(188)
; OTHER INFORMATION: Xaa = uncertain amino acid residue
; NAME/KEY: misc_feature
; LOCATION: (194)..(194)
; OTHER INFORMATION: Xaa = uncertain amino acid residue
; NAME/KEY: misc_feature
; LOCATION: (196)..(196)
; OTHER INFORMATION: Xaa = uncertain amino acid residue
; NAME/KEY: misc_feature
; LOCATION: (214)..(214)
; OTHER INFORMATION: Xaa = uncertain amino acid residue
; US-09-746-801A-61

```

```

Query Match
Best Local Similarity 51.4%; Score 36; DB 10; Length 324;
Pred. No. 78;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 2 NPPEKLLP 10
DB 237 NPPEKLLP 245

```

```

RESULT 13
US-09-815-242-11871
; Sequence 11871, Application US/09815242
; Patent No. US20020061569A1

```

```

; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlson, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 11871
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; US-09-815-242-11871

```

```

Query Match
Best Local Similarity 51.4%; Score 36; DB 10; Length 333;
Pred. No. 81;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

QY 3 PPVEKLLP 13
DB 260 PPVEKLLP 270

```

```

RESULT 14
US-09-815-242-5506
; Sequence 5506, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlson, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; TITLE OF INVENTION: Prokaryotes
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27

```

```

; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5506
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-5506

```

```

Query Match          51.4%; Score 36; DB 10; Length 401;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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```

OY 1 SNPPVEKLLP 10
    ||||: ||:|
DB 109 SNPPILPLIP 118

```

```

RESULT 15
US-09-815-242-12261
; Sequence 12261, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes In
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12261
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-815-242-12261

```

```

Query Match          51.4%; Score 36; DB 10; Length 401;
Best Local Similarity 60.0%; Pred. No. 1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

OY 1 SNPPVEKLLP 10
    ||||: ||:|
DB 109 SNPPILPLIP 118

```

Search completed: January 12, 2003, 04:19:15  
 Job time : 19 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 12, 2003, 04:12:01 ; Search time 40 Seconds  
(without alignments)  
33.647 Million cell updates/sec

Title: HANDENTERED  
Perfect score: 70  
Sequence: 1 snnpvexklplslk 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues  
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: p1r1:\*  
2: p1r2:\*  
3: p1r3:\*  
4: p1r4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	47	67.1	889	2 T47311	hypothetical prote
2	42	60.0	327	2 D70346	conserved hypothet
3	42	60.0	333	2 T29208	hypothetical prote
4	42	60.0	366	2 T47360	hypothetical prote
5	42	60.0	386	2 A39732	H+-transporting tw
6	42	60.0	450	2 G96749	hypothetical prote
7	42	60.0	663	2 T26835	hypothetical prote
8	42	60.0	1075	2 B96508	hypothetical prote
9	42	60.0	1350	2 T42697	hypothetical prote
10	41	58.6	376	2 S27976	H+-transporting tw
11	41	58.6	593	2 E81277	hypothetical prote
12	41	58.6	649	2 C81275	hypothetical prote
13	41	58.6	653	2 B81277	hypothetical prote
14	40	57.1	105	2 A12020	hypothetical prote
15	40	57.1	288	2 S18438	hypothetical prote
16	40	57.1	1115	2 T11614	sporulation protei
17	39	55.7	316	1 PWTCG	probable poly(A)-s
18	39	55.7	316	1 R5RT10	H+-transporting tw
19	39	55.7	316	1 R5RT10	acidic ribosomal p
20	39	55.7	317	1 R5HUP0	acidic ribosomal p
21	39	55.7	317	1 R5M810	acidic ribosomal p
22	39	55.7	317	1 R5PEP0	acidic ribosomal p
23	39	55.7	475	2 AE3036	slirheme synthase
24	39	55.7	488	2 F98249	slirheme synthase
25	39	55.7	653	2 A46362	amyloid precursor-
26	39	55.7	799	2 A82703	phosphoenolpyruvat
27	38	54.3	186	2 C82029	probable adhesin c
28	38	54.3	217	2 C86350	protein F8K.12 [I
29	38	54.3	284	2 F84590	probable heat shoc

30	38	54.3	292	2 A89823	conserved hypothet
31	38	54.3	312	2 T21351	hypothetical prote
32	38	54.3	315	2 E75382	hypothetical prote
33	38	54.3	358	1 PWRMG	H+-transporting tw
34	38	54.3	371	2 T13021	hypothetical prote
35	38	54.3	420	2 A84864	hypothetical prote
36	38	54.3	577	2 C84936	DNA primase [impor
37	38	54.3	738	2 F96701	hypothetical prote
38	38	54.3	1131	2 S22266	FUN30 protein - ye
39	38	54.3	2670	2 T37919	GCN1 homolog - fis
40	38	54.3	2672	2 A48126	translation activa
41	37	52.9	158	2 B90842	hypothetical prote
42	37	52.9	166	2 T27540	hypothetical prote
43	37	52.9	181	2 T14538	probable ethylene
44	37	52.9	227	2 A82008	hypothetical prote
45	37	52.9	283	2 A99967	hypothetical prote

ALIGNMENTS

RESULT 1  
T47311  
hypothetical protein T32A11.100 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C:Accession: T47311  
R:Reger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke  
submitted to the Protein Sequence Database, April 2000  
A:Reference number: Z24459  
A:Accession: T47311  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-889 <RIE>  
A:Cross-references: EMBL:AL138653  
A:Experimental source: cultivar Columbia; BAC clone T32A11  
C:Genetics:  
A:Map position: 3  
A:Introns: 88/3; 282/3; 455/3; 497/3; 547/3; 569/3; 607/3; 629/3; 667/3; 694/3; 716/3  
A:Note: T32A11.100

Query Match 67.1%; Score 47; DB 2; Length 889;  
Best Local Similarity 75.0%; Pred. No. 4.8;  
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
DB 552 SNPSVEKVLPLN 563

RESULT 2  
D70346  
conserved hypothetical protein aq\_512 - Aquifex aeolicus  
C:Species: Aquifex aeolicus  
C:Date: 08-May-1998 #sequence\_revision 08-May-1998 #text\_change 05-Nov-1999  
C:Accession: D70346  
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;  
V.  
Nature 392, 353-358, 1998  
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.  
A:Reference number: A70300; M0ID:9819666; PMID:9537320  
A:Accession: D70346  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-327 <NOF>  
A:Cross-references: GB:AE000693; NID:g2983148; PIDN:AAC06763.1; PID:g2983161; GB:AE00  
A:Experimental source: strain VFS  
C:Genetics:  
A:Gene: aq\_512

Query Match 60.0%; Score 42; DB 2; Length 327;  
Best Local Similarity 63.6%; Pred. No. 12;  
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 SNPEVKLLPL 11  
 ||||| : : :  
 DB 311 SNPEVKLLPL 321

## RESULT 3

T29208  
 hypothetical protein T20F5.4 - *Caenorhabditis elegans*  
 C:Species: *Caenorhabditis elegans*  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T29208  
 R:Du, Z.; Le, T.T.  
 submitted to the EMBL Data Library, November 1996  
 A:Description: The sequence of *C. elegans* cosmid T20F5.  
 A:Reference number: Z20588  
 A:Accession: T29208

A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-333 <DUZ>  
 A:Cross-references: EMBL:U00442; PIDN:AA37665.1; GSPDB:GN00019; CESP:T20F5.4  
 A:Experimental source: strain Bristol N2; clone T20F5  
 C:Genetics:  
 A:Gene: CESP:T20F5.4  
 A:Map position: 1  
 A:Introns: 35/3; 103/2; 177/2; 191/3; 240/3; 314/2

Query Match 60.0%; Score 42; DB 2; Length 333;  
 Best Local Similarity 53.8%; Pred. No. 12;  
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 NPPEVKLLPLSLK 14  
 :||| : ||| :  
 DB 272 SPVRRALPLSLK 284

## RESULT 4

T47360  
 hypothetical protein F7M19.30 - *Arabidopsis thaliana*  
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C>Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
 C:Accession: T47360  
 R:Nyakatura, G.; Farcman, B.; Dauner, D.; Sterr, W.; Holland, R.; Welchselgartner, M.;  
 Mayer, K.F.X.  
 submitted to the Protein Sequence Database, April 2000  
 A:Reference number: Z24458  
 A:Accession: T47360

A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-366 <NYA>  
 A:Cross-references: EMBL:AL138643  
 A:Experimental source: cultivar Columbia; BAC clone F7M19  
 C:Genetics:  
 A:Map position: 3  
 A:Introns: 98/3; 140/3; 189/3; 211/3; 245/3; 272/3; 299/3; 317/3  
 A:Note: F7M19.30

Query Match 60.0%; Score 42; DB 2; Length 366;  
 Best Local Similarity 75.0%; Pred. No. 14;  
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 SNPEVKLLPLS 12  
 || ||||| :  
 DB 194 SNQSVKLLPLN 205

## RESULT 5

A39732  
 H+-transporting two-sector ATPase (EC 3.6.3.14) gamma-2 chain precursor, chloroplast - *A*  
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C>Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 03-Jun-2002  
 C:Accession: A39732  
 R:Inohara, N.; Iwamoto, A.; Moriyama, Y.; Shimomura, S.; Maeda, M.; Futai, M.

J. Biol. Chem. 266, 7333-7338, 1991  
 A:Title: Two genes, atpC1 and atpC2, for the gamma subunit of *Arabidopsis thaliana* ch  
 A:Reference number: A39732; MUID:91210234; PMID:1826905  
 A:Accession: A39732

A:Molecule type: DNA  
 A:Residues: 1-386 <INO>  
 A:Cross-references: GB:M61741  
 A:Note: the authors translated the codon GAA for residue 192 as Asp, GAT for residue  
 C:Genetics:  
 A:Gene: atpC2  
 A:Introns: #status absent  
 C:Superfamily: H+-transporting ATP synthase gamma chain  
 C:Keywords: ATP biosynthesis; chloroplast; hydrolase; membrane-associated complex; th  
 F:1-60/Domain: transit peptide (chloroplast) #status predicted <TNP>  
 F:61-386/Product: H+-transporting ATP synthase gamma chain 2 #status predicted <MAT>  
 F:260-266/Dissulfide bonds: #status predicted

Query Match 60.0%; Score 42; DB 2; Length 386;  
 Best Local Similarity 57.1%; Pred. No. 15;  
 Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 SNPEVKLLPLSLK 14  
 :||| : ||||| :  
 DB 243 SDPVITRLPLSMK 256

## RESULT 6

G96749  
 hypothetical protein F28P22.27 [imported] - *Arabidopsis thaliana*  
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)  
 C>Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 17-May-2002  
 C:Accession: G96749  
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon  
 Chiu, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,  
 ansen, N.F.; Hughes, B.; Huizar, L.  
 Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,  
 C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maitl, R.; Marzia  
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo  
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A:Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.  
 A:Reference number: A86141; MUID:21016719; PMID:11130712  
 A:Accession: G96749

A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-450 <STO>  
 A:Cross-references: GB:AE005173; MID:96648174; PIDN:AAF21174.1; GSPDB:GN00141  
 C:Genetics:  
 A:Gene: F28P22.27  
 A:Map position: 1  
 C:Superfamily: kinase-related transforming protein; protein kinase homology

Query Match 60.0%; Score 42; DB 2; Length 450;  
 Best Local Similarity 75.0%; Pred. No. 17;  
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 SNPEVKLLPLS 12  
 :||| ||||| ||  
 DB 26 TNPEVKLLPLS 37

## RESULT 7

T26835  
 hypothetical protein Y43FA.1 - *Caenorhabditis elegans*  
 C:Species: *Caenorhabditis elegans*  
 C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
 C:Accession: T26835  
 R:Matthews, L.  
 submitted to the EMBL Data Library, September 1997  
 A:Reference number: Z20775  
 A:Accession: T26835

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA  
 A:Residues: 1-663 <MIL>  
 A:Cross-references: EMBL:Z99271; NID:e1062263; PIDN:CAB16471.1; GSPDB:GN00021; CESP:Y43F4  
 A:Experimental source: clone Y43F4A  
 C:Genetics:  
 A:Gene: CESP:Y43F4A.1  
 A:Map position: 3  
 A:Introns: 29/3; 120/2; 159/3; 187/2; 273/2; 310/3; 360/3; 393/2; 423/2; 446/2; 567/3

Query Match 60.0%; Score 42; DB 2; Length 663;  
 Best Local Similarity 50.0%; Pred. No. 27;  
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 SNPPVEKILPLSLK 14  
 ::::: ||:::  
 Db 60 TSPVEKEFAPLRIG 73

RESULT 8  
 B96508  
 hypothetical protein T12C22.16 [Imported] - Arabidopsis thaliana  
 C:Species: Arabidopsis thaliana (mouse-ear cress)  
 C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
 C:Accession: B96508  
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hultzer, L.  
 Nature 408, 816-820, 2000  
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maitl, R.; Marziani, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
 A:Reference number: A86141; MID:21016719; PMID:11130712  
 A:Accession: B96508  
 A>Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-1075 <STO>  
 A:Cross-references: GB:AE005173; NID:g8655999; PIDN:AAF78272.1; GSPDB:GN00141  
 C:Genetics:  
 A:Gene: T12C22.16  
 A:Map position: 1

Query Match 60.0%; Score 42; DB 2; Length 1075;  
 Best Local Similarity 75.0%; Pred. No. 46;  
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 SNPPVEKILPLSLK 12  
 ::::: ||:::  
 Db 569 SNOSEVEKILPLN 580

RESULT 9  
 T42697  
 hypothetical protein DKFZp434N035.1 - human (fragment)  
 N:Alternate names: hypothetical protein DKFZp434D0815.1; hypothetical protein DKFZp434I0141  
 C:Species: Homo sapiens (man)  
 C:Date: 11-Jan-2000 #sequence\_revision 11-Jan-2000 #text\_change 02-Sep-2000  
 C:Accession: T42697; T42651; T42672; T46321  
 R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
 submitted to the Protein Sequence Database, November 1999  
 A:Reference number: Z22232  
 A:Accession: T42697  
 A:Molecule type: mRNA  
 A:Residues: 1-1350 <POD>  
 A:Cross-references: EMBL:AL133040  
 A:Experimental source: adult testis; clone DKFZp434N035  
 R:Boeckler, H.; Boecker, M.; Brandt, P.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.  
 submitted to the Protein Sequence Database, November 1999  
 A:Reference number: Z22230  
 A:Accession: T42651  
 A:Molecule type: mRNA

A:Residues: 323-1350 <BLO1>  
 A:Cross-references: EMBL:AL133048  
 A:Experimental source: adult testis; clone DKFZp434D0815  
 A:Accession: T42672  
 A:Molecule type: mRNA  
 A:Residues: 435-1350 <BLO2>  
 A:Cross-references: EMBL:AL133072  
 A:Experimental source: adult testis; clone DKFZp434I0617  
 R:Duesterhoef, A.; Lauber, J.; Mewes, H.W.; Well, B.; Wiemann, S.  
 submitted to the Protein Sequence Database, January 2000  
 A:Reference number: Z23036  
 A:Accession: T46321  
 A:Molecule type: mRNA  
 A:Residues: 725-1350 <DUE>  
 A:Cross-references: EMBL:AL137622  
 A:Experimental source: adult testis; clone DKFZp434I2412  
 C:Genetics:  
 A:Note: DKFZp434N035.1; DKFZp434D0815.1; DKFZp434I0617.1; DKFZp434I2412.1  
 C:Superfamily: human retinoblastoma binding protein 2

Query Match 60.0%; Score 42; DB 2; Length 1350;  
 Best Local Similarity 77.8%; Pred. No. 59;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 PPVEKILPL 11  
 ::::: ||:::  
 Db 1033 PPLEKILPL 1041

RESULT 10  
 S27976  
 H+-transporting two-sector ATPase (EC 3.6.3.14) gamma chain precursor, chloroplast -  
 C:Species: Pisum sativum (garden pea)  
 C:Date: 17-Apr-1993 #sequence\_revision 17-Apr-1993 #text\_change 03-Jun-2002  
 C:Accession: S27976; S18951  
 R:Napier, J.A.; Hoeglund, A.S.; Plant, A.L.; Gray, J.C.  
 Plant Mol. Biol. 20, 737-741, 1992  
 A:Title: Chloroplast import of the precursor of the gamma subunit of pea chloroplast  
 A:Reference number: S27976; MID:93081734; PMID:1450388  
 A:Accession: S27976  
 A:Molecule type: mRNA  
 A:Residues: 1-376 <NAP>  
 A:Cross-references: EMBL:X63604; NID:g20653; PIDN:CAA45150.1; PID:g20654  
 C:Genetics:  
 A:Gene: atpC  
 C:Superfamily: H+-transporting ATP synthase gamma chain  
 C:Keywords: ATP biosynthesis; chloroplast; hydrolase; membrane-associated complex; th  
 F:1-52/Domain: transit peptide (chloroplast) #status predicted <TNP>  
 F:53-376/Product: H+-transporting ATP synthase gamma chain #status predicted <MAT>  
 F:250-256/Disulfide bonds: #status predicted

Query Match 58.6%; Score 41; DB 2; Length 376;  
 Best Local Similarity 64.3%; Pred. No. 21;  
 Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 SNPPVEKILPLSLK 14  
 ::::: ||:::  
 Db 233 SNPIIHLPLSPK 246

RESULT 11  
 E81277  
 hypothetical protein C11336 [Imported] - Campylobacter jejuni (strain NCTC 11168)  
 C:Species: Campylobacter jejuni  
 C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 03-Jun-2002  
 C:Accession: E81277  
 R:Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D.; Chl  
 C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Bar  
 Nature 403, 665-668, 2000  
 A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals  
 A:Reference number: A81250; MID:20150912; PMID:10688204  
 A:Accession: E81277  
 A>Status: preliminary

A:Molecule type: DNA  
 A:Residues: 1-593 <PAR>  
 A:Cross-references: GB:AL139078; GB:AL111168; NID:96968723; PIDN:CAB73763.1; PID:9696877  
 A:Experimental source: serotype O2, strain NCTC 11168  
 C:Genetics:  
 A:Gene: Cj1336  
 C:Superfamily: Campylobacter jejuni hypothetical protein Cj1337

Query Match 58.6%; Score 41; DB 2; Length 593;  
 Best Local Similarity 75.0%; Pred. No. 36;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 NPVEKLLPLSL 13  
 Db 427 NKPEKLEPLSL 438

RESULT 12  
 C81275  
 hypothetical protein Cj1318 [imported] - Campylobacter jejuni (strain NCTC 11168)  
 C:Species: Campylobacter jejuni  
 C>Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 03-Jun-2002  
 C:Accession: C81275  
 R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kelsey, J.M.; Churcher, C.; Basham, D.; Chilling  
 C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrett  
 Nature 403, 665-668, 2000  
 A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyf  
 A:Reference number: AB1250; MUID:20150912; PMID:10688204  
 A:Accession: C81275  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-649 <PAR>  
 A:Cross-references: GB:AL139078; GB:AL111168; NID:96968723; PIDN:CAB73745.1; PID:9696875  
 A:Experimental source: serotype O2, strain NCTC 11168  
 C:Genetics:  
 A:Gene: Cj1318  
 C:Superfamily: Campylobacter jejuni hypothetical protein Cj1337

Query Match 58.6%; Score 41; DB 2; Length 649;  
 Best Local Similarity 75.0%; Pred. No. 39;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 NPVEKLLPLSL 13  
 Db 483 NKPEKLEPLSL 494

RESULT 13  
 B81277  
 hypothetical protein Cj1333 [imported] - Campylobacter jejuni (strain NCTC 11168)  
 C:Species: Campylobacter jejuni  
 C>Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 03-Jun-2002  
 C:Accession: B81277  
 R:Parkhill, J.; Wren, B.W.; Mungall, K.; Kelsey, J.M.; Churcher, C.; Basham, D.; Chilling  
 C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVleet, A.; Whitehead, S.; Barrett  
 Nature 403, 665-668, 2000  
 A:Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hyf  
 A:Reference number: AB1250; MUID:20150912; PMID:10688204  
 A:Accession: B81277  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-653 <PAR>  
 A:Cross-references: GB:AL139078; GB:AL111168; NID:96968723; PIDN:CAB73760.1; PID:9696876  
 A:Experimental source: serotype O2, strain NCTC 11168  
 C:Genetics:  
 A:Gene: Cj1333  
 C:Superfamily: Campylobacter jejuni hypothetical protein Cj1337

Query Match 58.6%; Score 41; DB 2; Length 653;  
 Best Local Similarity 75.0%; Pred. No. 40;  
 Matches 9; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 NPVEKLLPLSL 13

Db 483 NKPEKLEPLSL 494

RESULT 14  
 AI2020  
 hypothetical protein all1719 [imported] - Nostoc sp. (strain PCC 7120)  
 C:Species: Nostoc sp.  
 A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120  
 C>Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 30-Jun-2002  
 C:Accession: AI2020  
 R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irigu  
 Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata  
 DNA Res. 8, 205-213, 2001  
 A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium  
 A:Reference number: AB1807; MUID:21595285; PMID:11759840  
 A:Accession: AI2020  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-105 <KUN>  
 A:Cross-references: GB:BA000019; PIDN:BA873418.1; PID:917130809; GSPDB:GN00179  
 A:Experimental source: strain PCC 7120  
 C:Genetics:  
 A:Gene: all1719

Query Match 57.1%; Score 40; DB 2; Length 105;  
 Best Local Similarity 58.3%; Pred. No. 7.7;  
 Matches 7; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy 3 PVEKLLPLSLK 14  
 Db 39 PVEKLLPLSLK 50

RESULT 15  
 S18438  
 sporulation protein spoIVFB - Bacillus subtilis  
 N:Alternate names: pro-sigma-K processing proteinase spoIVFB  
 C:Species: Bacillus subtilis  
 C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 15-Oct-1999  
 C:Accession: S18438; C69714  
 R:Cutting, S.; Roels, S.; Losick, R.  
 J. Mol. Biol. 221, 1237-1256, 1991  
 A:Title: Sporulation operon spoIVFB and the characterization of mutations that uncoupl  
 A:Reference number: S18437; MUID:92046062; PMID:1942049  
 A:Accession: S18438  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-288 <CUT>  
 A:Cross-references: EMBL:X59528; NID:940170; PIDN:CAA42107.1; PID:9580934  
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber  
 C.; Bron, S.; Brouillet, S.; Burschl, C.V.; Caldwell, B.; Capano, V.; Carter, N.M.;  
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabelt, C.; Ferrari,  
 Nature 380, 249-256, 1997  
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gal  
 lech, A.; J.; Hartwig, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M  
 Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino  
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau  
 Y. M.; Ogawa, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete  
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl  
 A:Authors: Schleich, S.; Schroeter, R.; Scottone, F.; Sekiguchi, J.; Sekowska, A.; Se  
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpiltra, P.; Tognoni, A.; Tosato, V.; Uchida  
 T.; Winters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida  
 A:Authors: Yoshikawa, H.F.; Zumsstein, E.; Yoshikawa, H.; Danchin, A.  
 A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis  
 A:Reference number: A69580; MUID:96044033; PMID:9384377  
 A:Accession: C69714  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-288 <KUN>  
 A:Cross-references: GB:Z99118; GB:AL009126; NID:92635200; PIDN:CAB14757.1; PID:el1840  
 A:Experimental source: strain 168  
 C:Genetics:

A:Gene: spoIVB  
A:Start codon: TTG  
C:Keywords: Transmembrane protein

Query Match 57.1%; Score 40; DB 2; Length 288;  
Best Local Similarity 61.5%; Pred. No. 24;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 NPYEKLLPLSLK 14  
| :|||||:  
Db 218 NRELEKLLPLTVK 230

Search completed: January 12, 2003, 04:18:11  
Job time : 48 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 12, 2003, 01:58:03 ; Search time 21 Seconds  
(without alignments)  
27.651 Million cell updates/sec

Title: HANDENTERED  
Perfect score: 70  
Sequence: 1 snppvek1p1slk 14

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues  
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	60.0	386	1	ATP2_ARATH
2	41	58.6	376	1	ATPC_PRA
3	40	57.1	288	1	SP4G_BACSU
4	40	57.1	1115	1	YAA4_SCHPO
5	39	55.7	117	1	SP21_PAEPO
6	39	55.7	309	1	RLAO_BOVIN
7	39	55.7	316	1	ATPG_SYNP6
8	39	55.7	316	1	RLAO_CHICK
9	39	55.7	317	1	RLAO_DROME
10	39	55.7	317	1	RLAO_HUMAN
11	39	55.7	317	1	RLAO_ICPU
12	39	55.7	317	1	RLAO_MOUSE
13	39	55.7	317	1	RLAO_RAT
14	39	55.7	653	1	APPL_MOUSE
15	38	54.3	311	1	RLAO_CAEEL
16	38	54.3	316	1	RLAO_PLAF8
17	38	54.3	358	1	ATPG_CHIRE
18	38	54.3	577	1	PRIM_BUCAI
19	38	54.3	1131	1	YAB8_YEAST
20	38	54.3	2670	1	YAO5_SCHPO
21	38	54.3	2672	1	GCN1_YEAST
22	37	52.9	219	1	SSL_DROME
23	37	52.9	282	1	YEDU_ECOLI
24	37	52.9	364	1	ATPG_SPROL
25	37	52.9	393	1	HVC3_HETER
26	37	52.9	394	1	LPXB_SYNY3
27	37	52.9	438	1	HVCS_HETER
28	37	52.9	461	1	HVCM_HETER
29	37	52.9	497	1	IRFS_MOUSE
30	37	52.9	1165	1	PEX6_PICPA
31	36.5	52.1	687	1	SRB4_YEAST
32	36.5	52.1	1181	1	NKX1_RAT
33	36	51.4	226	1	PRH1_HUMAN

34	36	51.4	283	1	YK26_YEAST	P36139 saccharomyc
35	36	51.4	301	1	NHAR_ECOLI	P10087 escherichia
36	36	51.4	314	1	TOP1_SFVKA	P16472 shope fibro
37	36	51.4	319	1	RLAO_BRARE	O9P9V0 brachydanio
38	36	51.4	373	1	ATP1_ARATH	O01908 arabidopsis
39	36	51.4	377	1	ATPG_TOBAC	P29790 nicotiana t
40	36	51.4	529	1	ACH2_HUMAN	Q15822 homo sapien
41	36	51.4	572	1	CY42_TRYBB	O99396 trypanosoma
42	36	51.4	1042	1	EF3_PNECA	P29551 pneumocysti
43	35	50.0	93	1	UGR1_HUMAN	O96P11 homo sapien
44	35	50.0	110	1	RPOZ_MYCLE	O9CG66 mycobacteri
45	35	50.0	110	1	RPOZ_MYCTU	P71660 mycobacteri

## ALIGNMENTS

RESULT 1  
ATP2\_ARATH STANDARD; PRT; 386 AA.  
AC 001909;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 15-JUN-2002 (Rel. 41, Last sequence update)  
DE ATP synthase gamma chain 2, chloroplast precursor (EC 3.6.3.14).  
GN ATPC2 OR AT1G15700 OR F7H2.4.  
OS Arabidopsis thaliana (Mouse-ear cress).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.  
OX NCBI\_TaxID=3702;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=91210234; PubMed=1826905;  
RA Itohara N., Iwamoto A., Moriyama Y., Shimomura S., Maeda M.,  
RA Futai M.,  
RT "Two genes, atpC1 and atpC2, for the gamma subunit of Arabidopsis  
thaliana chloroplast ATP synthase.";  
RL J. Biol. Chem. 266:7333-7338(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. Columbia;  
RX MEDLINE=21016719; PubMed=11130712;  
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,  
RA White O., Alonso J., Holt T., Bowman C.L., Brooks S.Y.,  
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,  
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,  
RA Dunn P., Elgu P., Feldblum T.V., Feng J.-D., Fong B., Fujii C.Y.,  
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,  
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,  
RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,  
RA Langin-Hooper S., Lee A., Lee J.M., Lenz A., Li J.H., Li Y.-P.,  
RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Maizel R., Marzilli A.,  
RA Maltischer J., Miranda M., Nguyen M., Nietman W.C., Osborne B.I.,  
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,  
RA Uterback T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,  
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,  
RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis  
thaliana.";  
RL Nature 408:816-820(2000).  
CC - FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON  
GRADIENT ACROSS THE MEMBRANE. THE GAMMA CHAIN IS BELIEVED TO BE  
IMPORTANT IN REGULATING ATPASE ACTIVITY AND THE FLOW OF PROTONS  
THROUGH THE CF(0) COMPLEX.  
CC - CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (in) = ADP + phosphate +  
H(+) (out).  
CC - SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC  
CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE  
SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)  
HAS THREE MAIN SUBUNITS: A, B AND C.  
CC - SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.

CC -1- INDUCTION: BY LIGHT.  
CC -1- SIMILARITY: BELONGS TO THE ATPASE GAMMA CHAIN FAMILY.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
CC DR EMBL: M61742: AAA32833.1; -  
CC DR EMBL: AC034256: AAF82140.1; -  
CC DR PIR: A39732: A39732.  
CC DR InterPro: IPR000131: ATPase\_gamma.  
CC DR Pfam: PF00231: ATP-synt. 1.  
CC DR PRINTS: PR00126: ATPASEGAMMA.  
CC DR TIGREAFMS: TIGR01146: ATPsyn\_F1gamma; 1.  
CC DR PROSITE: P800153: ATPASE\_GAMMA.1.  
CC KW ATP synthetase; Chloroplast; Thylakoid; Membrane; CF(1);  
CC Hydrolyase; Hydrogen ion transport; Transil peptide; Multigene family.  
CC FT TRANSIT 1 60 CHLOROPLAST (BY SIMILARITY).  
CC FT CHAIN 61 386 ATP SYNTHASE GAMMA CHAIN 2.  
CC FT ACT\_SITE 149 149 BY SIMILARITY.  
CC FT DISULFID 260 266 BY SIMILARITY.  
CC SQ SEQUENCE 386 AA: 42679 MW; 2BDC2EF47EBCAC3A CRC64;  
CC  
CC Query Match 60.0%; Score 42; DB 1; Length 386;  
CC Best Local Similarity 57.1%; Pred. No. 6.3;  
CC Matches 8; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
CC  
CC QY 1 SNPPYEKLPLSLK 14  
CC I:I: |||||:|  
CC Db 243 SDPVHTLPLSMK 256  
CC  
CC RESULT 2  
CC ATPG\_PEA  
CC ID ATPG\_PEA STANDARD: PRT; 376 AA.  
CC AC P28552;  
CC DT 01-DEC-1992 (Rel. 24, Created)  
CC DM 01-DEC-1992 (Rel. 24, Last sequence update)  
CC DT 15-JUN-2002 (Rel. 41, Last annotation update)  
CC DE ATP synthase gamma chain, chloroplast precursor (EC 3.6.3.14).  
CC OS Arabidopsis thaliana (Garden pea).  
CC GN P15um salivum (Garden pea).  
CC CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
CC OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
CC OC eucosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.  
CC NCBI\_TaxID=3888;  
CC [1]  
CC RX MEDLINE=93081734; PubMed=1450388;  
CC RA Napier J.A., Hglund A.S., Plant A.L., Gray J.C.;  
CC RT "Chloroplast import of the precursor of the gamma subunit of pea  
CC chloroplast ATP synthase."  
CC RL Plant Mol. Biol. 20:737-741(1992).  
CC CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON  
CC GRADIENT ACROSS THE MEMBRANE. THE GAMMA CHAIN IS BELIEVED TO BE  
CC IMPORTANT IN REGULATING ATPASE ACTIVITY AND THE FLOW OF PROTONS  
CC THROUGH THE CF(0) COMPLEX.  
CC CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+)(in) = ADP + phosphate +  
CC H(+)(Out).  
CC CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC  
CC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE  
CC SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0)  
CC HAS THREE MAIN SUBUNITS: Chloroplast thylakoid membrane.  
CC CC -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.  
CC CC -1- SIMILARITY: BELONGS TO THE ATPASE GAMMA CHAIN FAMILY.  
CC  
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CC -----
CC EMBL, X63604; CAA45150.1; -.
CC DR PIR; S18951; S18951.
CC DR PIR; S27976; S27976.
CC DR InterPro; IPR000131; ATPase_gamma.
CC DR InterPro; IPR001230; Prenyl_site.
CC DR Pfam; PF00231; ATP-synt.1.
CC DR PRINTS; PR00126; ATPASGAMMA.
CC DR TIGRFSMS; TIGR01146; Arpsyn_F1gamma; 1.
CC DR PROSITE; PS00153; ATPASE_GAMMA; FALSE_NEG.
CC KM ATP synthesis; Chloroplast; Thylakoid Membrane; CF(1);
CC KW Hydrolyase; Hydrogen ion transport; Transit peptide.
CC FT TRANSIT 1 52 CHLOROPLAST (BY SIMILARITY).
CC FT CHAIN 53 376 ATP SYNTHASE GAMMA CHAIN.
CC FT ACT_SITE 133 133 BY SIMILARITY.
CC FT DISULFID 250 256 BY SIMILARITY.
CC SO SEQUENCE 376 AA; 41410 MW; 6976834B12F3CD18 CNC64;

Query Match 58.6%; Score 41; DB 1; Length 376;
Best Local Similarity 64.3%; Pred. NO. 9.2;
Matches 9; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 SNPVEKLLPLSLK 14
Db 233 SNPIHTLLPLSPK 246

RESULT 3
SP4G_BACSU
ID SP4G_BACSU STANDARD. PRT: 288 AA.
AC P26937;.
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Stage IV sporulation protein FB (EC 3.4.24.-).
GN SPO1VEF OR BOEF.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=92046062; PubMed=1942049;
RA Cutting S.M., Koels S., Losick R.;
RT "Sporulation operon spoIVF and the characterization of mutations that
RT uncouple mother-cell from forespore gene expression in Bacillus
RT subtilis.";
RL J. Mol. Biol. 221:1237-1256(1991).
[2]
RN RP MUTAGENESIS OF HIS-43; GLU-44 AND HIS-47.
RX MEDLINE=20270168; PubMed=10809718;
RA Yu Y.-T., Kroos L.;
RT "Evidence that SpoIVFB is a novel type of membrane metalloprotease
RT governing intercompartmental communication during Bacillus subtilis
RT sporulation.";
RL J. Bacteriol. 182:3305-3309(2000).
CC -1- FUNCTION: IMPLICATED IN THE COUPLING OF MOTHER CELL TO FORESPORE
CC GENE EXPRESSION. REQUIRED FOR SPORE FORMATION. PROBABLE
CC PROTEOLYTIC THAT PROCESSES THE PRO-SIGA K FACTOR.
CC -1- SUBUNIT: FORMS AN HETERODIMER WITH SPO1VEA (PROBABLE).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Outer membrane
CC surrounding the forespore protoplast (probable).
CC -1- DEVELOPMENTAL STAGE: TRANSCRIBED DURING THE STAGE II, BUT IS
CC NOT REQUIRED UNTIL THE STAGE IV OF SPOURATION.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M50B.
CC -----
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DR EMBL: X59528; CAA42107.1; -;  
DR EMBL: Z99118; CAB14757.1; -;  
DR PIR: S18438; S18438.  
DR MEROPS: M50.002; -;  
DR Subtilisin; BG10332; spoIIVB.  
KM Hydrolyase; Metalloprotease; Zinc; Sporulation; Transmembrane;  
KW Complete proteome.  
FT DOMAIN 1 10 MOTHER-CELL CYTOPLASM (PROBABLE).  
FT TRANSMEM 11 30 POTENTIAL.  
FT DOMAIN 31 31 FORESPORE INTERMEMBRANE SPACE (PROBABLE).  
FT TRANSMEM 32 56 POTENTIAL.  
FT DOMAIN 57 83 MOTHER-CELL CYTOPLASM (PROBABLE).  
FT TRANSMEM 84 105 POTENTIAL.  
FT TRANSMEM 106 128 FORESPORE INTERMEMBRANE SPACE (PROBABLE).  
FT TRANSMEM 127 146 POTENTIAL.  
FT DOMAIN 147 161 MOTHER-CELL CYTOPLASM (PROBABLE).  
FT TRANSMEM 162 178 POTENTIAL.  
FT DOMAIN 179 179 FORESPORE INTERMEMBRANE SPACE (PROBABLE).  
FT TRANSMEM 180 199 POTENTIAL.  
FT DOMAIN 200 288 MOTHER-CELL CYTOPLASM (PROBABLE).  
FT METAL 43 43 ZINC (CATALYTIC) (PROBABLE).  
FT ACT\_SITE 44 44 ZINC (CATALYTIC) (PROBABLE).  
FT METAL 47 47 ZINC (CATALYTIC) (PROBABLE).  
FT MUTAGEN 43 43 H->F: LOSS OF ACTIVITY.  
FT MUTAGEN 44 44 E->A/O: LOSS OF ACTIVITY.  
FT MUTAGEN 44 44 E->D: PARTIAL ACTIVITY.  
FT MUTAGEN 47 47 H->F: LOSS OF ACTIVITY.  
SQ SEQUENCE 288 AA; 33640 MW; 81DB758DC215C916 CRC64;

Query Match 57.18; Score 40; DB 1; Length 288;  
Best Local Similarity 61.58; Pred. No. 10;  
Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 2 NPEVKLPLSLK 14  
| :|||||:|  
Db 218 NREKLPLPLTVK 230

RESULT 4  
YAA4\_SCHPO STANDARD; PRT; 1115 AA.  
ID YAA4\_SCHPO  
AC 009798;  
DT 01-NOV-1995 (Rel. 32, Created)  
DT 01-NOV-1995 (Rel. 32, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Hypothetical protein C2267.04 in chromosome I.  
GN SPAC2267.04  
OS Schizosaccharomyces pombe (Fission yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomycetes.  
OX NCBI\_TaxID=4896;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=972;  
RX MEDLINE=21848401; PubMed=11859360;  
RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
RA Spouris J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,  
RA Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
RA Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K.,  
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabbittowitch E.,  
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,  
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,  
RA Wellens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
RA Gabel C., Fuchs M., Fritz C., Holzer E., Moestl D., Hilbert H.,  
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,  
RA Eger P., Zimmermann W., Medler H., Mamut R., Purnelle B.,  
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaire V., Mottier S.,  
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
RA Lucas M., Rochet M., Gallardin C., Tallada V.A., Garzon A., Thode G.,  
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
RA Cervetti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,  
RA Sinapovskii G.V., Ussery D., Barrell B.G., Nurse P.;  
RT "The genome sequence of Schizosaccharomyces pombe."  
RL Nature 415:871-880(2002).  
CC -1- SIMILARITY: TO YEAST PAN2 AND TO C. ELGANS F31E3.4.

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DR EMBL: Z54328; CAA91128.1; -;  
DR Interpro: IPR000520; Exonuclease.  
DR Interpro: IPR001394; UCH-2.  
DR Pfam: PF00443; UCH-2; 1.  
DR Pfam: PF00929; Exonuclease; 1.  
DR SMART: SM00479; EXOIII; 1.  
DR SMART: PS50235; UCH\_2\_3; 1.  
DR PROSITE: PS50235; UCH\_2\_3; 1.  
KM Hypothetical protein.  
SQ SEQUENCE 1115 AA; 126919 MW; EEF6F15E1897269D CRC64;

Query Match 57.18; Score 40; DB 1; Length 1115;  
Best Local Similarity 54.58; Pred. No. 44;  
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;  
QY 2 NPEVKLPLSLK 12  
| | : | : | : |  
Db 866 NPEVKLPLSLK 876  
RESULT 5  
SP21\_PAEPO STANDARD; PRT; 1117 AA.  
ID SP21\_PAEPO  
AC 032720;  
DT 15-JUL-1998 (Rel. 36, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE Anti-sigma F factor antagonist (Stage II sporulation protein AA).  
GN SPOIIIA.  
OS Paenibacillus polymyxa (Bacillus polymyxa).  
OC Bacteria; Firmicutes; Bacillales; Paenibacillaceae; Paenibacillus.  
OX NCBI\_TaxID=1406;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=DSM 36;  
RX MEDLINE=9740954; PubMed=9266669;  
RA Park S.G., Yuckin M.D.;  
RT "Sequencing and phylogenetic analysis of the spoIIA operon from  
RT diverse Bacillus and Paenibacillus species."  
RL Gene 194:25-33(1997).  
CC -1- FUNCTION: IN THE PHOSPHORYLATED FORM IT COULD ACT AS AN ANTI-ANTI-  
CC SIGMA FACTOR THAT COUNTERACTS SPOIIAB AND THUS RELEASES SIGMA F  
CC FROM INHIBITION (BY SIMILARITY).  
CC -1- PFM: PHOSPHORYLATED BY SPOIIAB ON A SERINE RESIDUE (BY  
CC SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE ANTI-SIGMA-FACTOR ANTAGONIST FAMILY.  
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EMBL: L47358; AAB81184.1; -  
 HSP: F10727; 1A02.  
 InterPro: IPR003658; Antisig\_antgst.  
 InterPro: IPR002645; STAS.  
 Pfam: PF01740; STAS; 1.  
 ProDom: PD005210; Antisig\_antgst; 1.  
 TIGRFAMs: TIGR00377; ant\_ant\_sig; 1.  
 PROSITE: PS50801; STAS; 1.  
 Sporulation: Phosphorylation.  
 KW DOMAIN 3  
 FT MOD\_RES 58  
 SEQUENCE 117 AA; 13341 MW; 7D66D2AABD788B0A CRC64;  
 PHOSPHORYLATION (BY SIMILARITY).

Query Match 55.7%; Score 39; DB 1; Length 117;  
 Best Local Similarity 63.6%; Pred. No. 6;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 NPPEVKLPLS 12  
 DB 84 NPPEVKLPLS 94

RESULT 6  
 ID BLAO\_BOVIN STANDARD; PRT; 309 AA.  
 AC 095140; 018788; Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-1998 (Rel. 36, Last sequence update)  
 DT 15-JUL-1998 (Rel. 36, Last annotation update)  
 DE 60S acidic ribosomal protein P0 (L10E) (Fragment).  
 GN RPLP0.  
 OS Bos taurus (bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 [1]  
 RP SEQUENCE OF 1-50 FROM N.A.  
 RC TISSUE=Adrenal cortex;  
 RA Mandiriot S.J., Pepper M.S.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 [2]  
 RP SEQUENCE OF 8-309 FROM N.A.  
 RC TISSUE=Adrenal cortex;  
 RA Mandiriot S.J., Pepper M.S.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
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 RA Mandiriot S.J., Pepper M.S.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
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 RA Mandiriot S.J., Pepper M.S.;  
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 RA Mandiriot S.J., Pepper M.S.;  
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 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
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 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 [33]  
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 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 [34]  
 RP TISSUE=Adrenal cortex;  
 RA Mandiriot S.J., Pepper M.S.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
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 RP TISSUE=Adrenal cortex;  
 RA Mandiriot S.J., Pepper M.S.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
 [36]  
 RP TISSUE=Adrenal cortex;  
 RA Mandiriot S.J., Pepper M.S.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
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 RP TISSUE=Adrenal cortex;  
 RA Mandiriot S.J., Pepper M.S.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
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 RP TISSUE=Adrenal cortex;  
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 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
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 RA Mandiriot S.J., Pepper M.S.;  
 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
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 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
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 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
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 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.  
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 RP TISSUE=Adrenal cortex;  
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 RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.

Ribosomal protein; Phosphorylation.  
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Query Match 55.7%; Score 39; DB 1; Length 309;  
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 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SNPEVKLPL 10  
 DB 62 SNPEVKLPL 71

RESULT 7  
 ID ATPG\_SYN6 STANDARD; PRT; 316 AA.  
 AC P08450; 018788; Created)  
 DT 01-AUG-1988 (Rel. 08, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE ATP synthase gamma chain (EC 3.6.3.14).  
 GN ATPG OR ATPC.  
 OS Synechococcus sp. (strain PCC 6301) (Anacystis nidulans).  
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.  
 OX NCBI\_TaxID=1139;  
 [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=87311713; PubMed=3041005;  
 RX Cozens A.L., Walker J.E.;  
 RT "The organization and sequence of the genes for ATP synthase subunits in the cyanobacterium Synechococcus 6301. Support for an endosymbiotic origin of chloroplasts."  
 RL J. Mol. Biol. 194:359-383(1987).  
 [2]  
 RP SEQUENCE OF 306-316 FROM N.A.  
 RX MEDLINE=88326273; PubMed=2843173;  
 RA Cozens A.L., Walker J.E.;  
 RT "Expression of a gene encoding a novel ferredoxin in the cyanobacterium Synechococcus 6301."  
 RL Biochem. J. 252:563-569(1988).  
 [3]  
 RP FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON GRADIENT ACROSS THE MEMBRANE. THE GAMMA CHAIN IS BELIEVED TO BE IMPORTANT IN REGULATING ATPASE ACTIVITY AND THE FLOW OF PROTONS THROUGH THE CF(0) COMPLEX.  
 CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate + H(+) (Out).  
 CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL. CF(1) HAS FIVE SUBUNITS: ALPHA(3), BETA(3), GAMMA(1), DELTA(1), EPSILON(1). CF(0) HAS THREE MAIN SUBUNITS: A, B AND C.  
 CC -1- SIMILARITY: BELONGS TO THE ATPASE GAMMA CHAIN FAMILY.  
 CC -----  
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EMBL: X03502; CAA28929.1; -  
 PIR: S10832; PWYCG.  
 InterPro: IPR000131; ATPase\_gamma.  
 Pfam: PF00231; ATP-synt; 1.  
 PRINTS: PR00126; ATPASGAMMA.  
 TIGRFAMs: TIGR01146; ATPSYN\_F1gamma; 1.  
 PROSITE: PS00153; ATPASE\_GAMMA; 1.  
 KW ATP synthetase; CF(1); Hydrogen ion transport; Hydrolyase.  
 SEQUENCE 316 AA; 34806 MW; 7451EB6D23DAD9DB CRC64;

Query Match 55.7%; Score 39; DB 1; Length 316;  
 Best Local Similarity 72.7%; Pred. No. 17;  
 Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 SNPEVKLPL 11  
 DB 183 SNPEVKLPL 193

RESULT 8  
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 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 01-OCT-1996 (Rel. 34, Last annotation update)  
 DE 60S acidic ribosomal protein P0 (L10E).  
 GN RPLP0.  
 OS Gallus gallus (Chicken).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 OC Gallus.  
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 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-White leghorn; TISSUE-Liver;  
 RX MEDLINE=96057559; PubMed=7549959;  
 RA Wang H., Meury L., Plasmoneault S., Morais R.;  
 RT "Chicken acidic ribosomal phosphoprotein P0: Isolation and molecular  
 RT characterization of cDNA clones.";  
 RL Biochem. Mol. Biol. Int. 36:595-604(1995).  
 CC -1- FUNCTION: RIBOSOMAL PROTEIN P0 IS THE FUNCTIONAL EQUIVALENT  
 CC OF E.COLI PROTEIN L10.  
 CC -1- SUBUNIT: P0 FORMS A PENTAMERIC COMPLEX BY INTERACTION WITH  
 CC DIMERS OF P1 AND P2.  
 CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.  
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 DR Pfam: PF00428; 60S\_Ribosomal; 1.  
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 KM Ribosomal protein; Phosphorylation.  
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 Best Local Similarity 70.0%; Pred. No. 17;  
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SNPEVKLPL 10  
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 AC P19889; O9VNV9;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE 60S acidic ribosomal protein P0 (Deoxyribonuclease (Apyriminic or  
 DE apyrimidinyl)) (EC 4.2.99.18) (Apyrimidin-apyrimidin endonuclease).  
 GN RBP0 OR APE OR AP3 OR CG7490.  
 OS Drosophila melanogaster (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;  
 OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;  
 OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxID=7227;  
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 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89261760; PubMed=2471063;  
 RA Kelley M.R., Venugopal S., Harless J., Deutsch W.A.;  
 RT "Antibody to a human DNA repair protein allows for cloning of a  
 RT Mol. Cell. Biol. 9:965-973(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Berkeley;  
 RX MEDLINE=20196006; PubMed=10731132;  
 RA Adams M.D., Celisner S.E., Holt R.A., Evans C.A., Gocayne J.D.,  
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 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,  
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,  
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;  
 RT "The genome sequence of Drosophila melanogaster.";  
 RL Science 287:2185-2195(2000).  
 RN [3]  
 RP SIMILARITY TO RIBOSOMAL PROTEIN P0.  
 RX MEDLINE=9136151; PubMed=1870984;  
 RA Grabowski D.T., Deutsch W.A., Derda D., Kelley M.R.;  
 RT "Drosophila AP3, a presumptive DNA repair protein, is homologous to  
 RT human ribosomal associated protein P0.";  
 RL Nucleic Acids Res. 19:4297-4297(1991).  
 RN [4]  
 RP DNA REPAIR ACTIVITY.  
 RX MEDLINE=97086697; PubMed=8932386;  
 RA Yacoub A., Kelley M.R., Deutsch W.A.;  
 RT "Drosophila ribosomal protein P0 contains apurinic/apyrimidinic  
 RT endonuclease activity.";  
 RL Nucleic Acids Res. 24:4298-4303(1996).  
 CC -1- FUNCTION: RIBOSOMAL PROTEIN P0 IS THE FUNCTIONAL EQUIVALENT  
 CC OF E.COLI PROTEIN L10.  
 CC -1- CATALYTIC ACTIVITY: The C-O-P bond 3' to the apurinic or  
 CC apyrimidinic site in DNA is broken by a beta-elimination reaction,  
 CC leaving a 3'-terminal unsaturated sugar and a product with a  
 CC terminal 5'-phosphate.  
 CC -1- SUBUNIT: P0 FORMS A PENTAMERIC COMPLEX BY INTERACTION WITH  
 CC DIMERS OF P1 AND P2 (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Nuclear and cytoplasmic.

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CC      -1- SUBUNIT: P0 FORMS A PENTAMERIC COMPLEX BY INTERACTION WITH
CC      DIMERS OF P1 AND P2.
CC      -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
CC
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CC      or send an email to license@isb-sib.ch).
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CC      DR      EMBL: AC004263; AAC05176.1; -
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CC      DR      EMBL: BC000345; AAH00345.1; -
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CC      DR      EMBL: BC001127; AAH01127.1; -
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CC      DR      PIR: A27125; R5HUP0
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CC      DR      MIM: 180510; -
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CC      DR      InterPro: IPR001790; Ribosomal_L10.
CC      DR      Pfam: PF00428; 60s_rribosomal; 1.
CC      DR      Pfam: PF00466; Ribosomal_L10; 1.
CC      KW      Ribosomal protein; Phosphorylation.
CC      FT      CONFLICT 246 246 K -> E (IN REF. 3; AAH01127).
CC      SQ      SEQUENCE 317 AA: 34273 MW: 255AD2571C51199 CRC64;
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CC      Query Match          55.7%; Score 39; DB 1; Length 317;
CC      Best Local Similarity 70.0%; Pred. NO. 17;
CC      Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0.
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CC      Qy      1 SNPEPKLIP 10
CC              :||:|||||
CC      Db      71 NNPALEKLLP 80
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CC      RESULT 11
CC      RLAO ICTPU
CC      ID      RLAO ICTPU      STANDARD:      PRT;      317 AA.
CC      AC      Q90YX1;
CC      DT      15-JUN-2002 (Rel. 41, Created)
CC      DT      15-JUN-2002 (Rel. 41, Last sequence update)
CC      DT      15-JUN-2002 (Rel. 41, Last annotation update)
CC      DE      60s acidic ribosomal protein P0 (L10P).
CC      GN      RPLP0.
CC      OS      Ictalarus punctatus (Channel catfish).
CC      OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC      OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
CC      OC      Ictaluridae; Ictalurus.
CC      CX      NCBI_Taxid=7998;
CC      RN      [1]
CC      RP      SEQUENCE FROM N.A.
CC      RA      Patterson A.P., Karsi A., Liu Z.-J.;
CC      RT      "Translational machinery of channel catfish: II. Complementary DNA and
CC      RT      expression of the complete set of 47 60S ribosomal proteins.";
CC      RL      Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC      -1- FUNCTION: RIBOSOMAL PROTEIN P0 IS THE FUNCTIONAL EQUIVALENT
CC      OF E.COLI PROTEIN L10.
CC      -1- SUBUNIT: P0 FORMS A PENTAMERIC COMPLEX BY INTERACTION WITH
CC      DIMERS OF P1 AND P2 (BY SIMILARITY).
CC      -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
CC

```

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CC -----  
CC EMBL; AF401551; AAK95123.1; -  
CC InterPro: IPR001813; 60S\_ribosomal.  
CC InterPro: IPR001790; Ribosomal\_L10.  
CC Pfam; PF00428; 60S\_ribosomal\_1.  
CC Pfam; PF00466; Ribosomal\_L10; 1.  
CC Riboosomal protein; Phosphorylation.  
CC SEQUENCE 317 AA; 34902 MW; 13E2FA0C08EE82AD CRC64;  
CC

Query Match 55.7%; Score 39; DB 1; Length 317;  
Best Local Similarity 70.0%; Pred. No. 17;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 SNPPVKLLP 10  
Db 71 NNPALEKLLP 80  
:|:|||||

RESULT 12  
ID RLAD\_MOUSE STANDARD; PRT; 317 AA.  
AC P14869;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 15-JUN-2002 (Rel. 41, Last annotation update)  
DE 60S acidic ribosomal protein P0 (L10E).  
GN RPLP0 OR ARP.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89366686; PubMed=2771657;  
RA Krowczynska A.M., Coutts M., Makrides S., Braverman G.;  
RT "The mouse homologue of the human acidic ribosomal phosphoprotein P0:  
RT a highly conserved polypeptide that is under translational control.";  
RL Nucleic Acids Res. 17:6408-6408(1989).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J;  
RX MEDLINE=21083660; PubMed=11217851;  
RA Kawai T., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Atakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Atzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.,  
RA Saito T., Okazaki Y., Gotohori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,  
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
RA Schirral L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsi G.,  
RA Blake J., Boffelli D., Bojuno M., Carlini P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F.,  
RA Suzuki H., Teyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
RA Wyszewski B., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,  
RA Hayashizaki Y.,  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
CC -1- FUNCTION: RIBOSOMAL PROTEIN P0 IS THE FUNCTIONAL EQUIVALENT  
CC OF E.COLI PROTEIN L10.  
CC -1- SUBUNIT: P0 FORMS A PENTAMERIC COMPLEX BY INTERACTION WITH  
CC DIMERS OF P1 AND P2.

CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.  
CC -----  
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CC -----  
CC EMBL; X15067; CAA33338.1; -  
CC EMBL; AK010267; BAB26807.1; -  
CC EMBL; AK012606; BAB28352.1; -  
CC PIR; S05305; R5MS10.  
CC MGD; MGI:88066; Ardp.  
CC InterPro: IPR001813; 60S\_ribosomal.  
CC InterPro: IPR001790; Ribosomal\_L10.  
CC Pfam; PF00428; 60S\_ribosomal\_1.  
CC Pfam; PF00466; Ribosomal\_L10; 1.  
CC Riboosomal protein; Phosphorylation.  
CC SEQUENCE 317 AA; 34216 MW; 7985E1D7B235EAD0 CRC64;  
CC

Query Match 55.7%; Score 39; DB 1; Length 317;  
Best Local Similarity 70.0%; Pred. No. 17;  
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Oy 1 SNPPVKLLP 10  
Db 71 NNPALEKLLP 80  
:|:|||||

RESULT 13  
ID RLAD\_RAT STANDARD; PRT; 317 AA.  
AC P19945;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DT 01-OCT-1996 (Rel. 34, Last annotation update)  
DE 60S acidic ribosomal protein P0 (L10E).  
GN RPLP0.  
GN Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Liver;  
RX MEDLINE=92075759; PubMed=1742361;  
RA Wool I.G., Chan Y.-L., Glueck A., Suzuki K.;  
RT "The primary structure of rat ribosomal proteins P0, P1, and P2 and a  
RT proposal for a uniform nomenclature for mammalian and yeast ribosomal  
RL proteins.";  
RL Biochimie 73:861-870(1991).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Myeloid;  
RX Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.  
RL Submitted (JAN-1994) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: RIBOSOMAL PROTEIN P0 IS THE FUNCTIONAL EQUIVALENT  
CC OF E.COLI PROTEIN L10.  
CC -1- SUBUNIT: P0 FORMS A PENTAMERIC COMPLEX BY INTERACTION WITH  
CC DIMERS OF P1 AND P2.  
CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.  
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CC -----  
CC EMBL; X15096; CAA33199.1; -

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DR EMBL: Z29530; CAAB2647.1; -
DR PIR: S08021; RSRT10.
DR PIR: A48397; A48397.
DR PIR: S41396; S41396.
DR InterPro: IPR001813; 60s_ribosomal.
DR InterPro: IPR001790; Ribosomal_L10.
DR Pfam: PF00428; 60s_ribosomal_L10.
DR Pfam: PF00466; Ribosomal_L10; 1.
KW Ribosomal protein; Phosphorylation.
FT CONFLICT 281 V -> L (IN REF. 1).
FT CONFLICT 287 A -> L (IN REF. 1).
FT CONFLICT 294 MISSING (IN REF. 1).
SO SEQUENCE 317 AA; 34215 MW; 7B842971C0E027EC CRC64;

Query Match
Best Local Similarity 55.7%; Score 39; DB 1; Length 317;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 SNPPVKLLP 10
DB 71 NNPALEKLP 80

RESULT 14
APPL_MOUSE STANDARD; PRT; 653 AA.
ID 003157;
AC 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DE 01-JUN-1994 (Rel. 29, Last annotation update)
DE Amyloid-like protein 1 precursor (APLP).
GN APLP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid-10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Brain;
RA MEDLINE-9306322; PubMed-1279693;
RA Masco W., Bupp K., Magendantz M., Gussella J.F., Tanzi R.E.,
RA Solomon F.;
RT "Identification of a mouse brain cDNA that encodes a protein related
RT to the Alzheimer disease-associated amyloid beta protein precursor.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:10758-10762(1992).
-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. MAY BE PROCESSED
IN THE GOLGI COMPLEX; HOWEVER, IT IS NOT YET CLEAR WHETHER APLP
IS SECRETED.
CC -1- SIMILARITY: BELONGS TO THE APP FAMILY.
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CC
CC EMBL: L04538; AAA37247.1; -
DR PIR: A46362; A46362.
DR HSSP: P05067; IAMP.
DR MGP: MGI:88046; APLP1.
DR InterPro: IPR001868; A4_APP.
DR Pfam: PF02177; A4_EXTRA; 1.
DR PRINTS: PR00203; AMYLOIDA.
DR SMART: SM00006; A4_EXTRA; 1.
DR PROSITE: PS00319; A4_EXTRA; 1.
DR PROSITE: PS00320; A4_INTRA; 1.
DR Glycoprotein; Transmembrane; Signal.
FT SIGNAL 1 20
FT CHAIN 21 653
FT DOMAIN 21 583
FT TRANSMEM 584 606
FT AMYLOID-LIKE PROTEIN 1.
FT EXTRACELLULAR (POTENTIAL).
FT POTENTIAL.

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FT DOMAIN 607 653
FT DOMAIN 643 646
FT DOMAIN 263 271
FT CARBOHYD 464 464
FT CARBOHYD 354 354
SO SEQUENCE 653 AA; 72751 MW; 56516DC3EA40E4B0 CRC64;

Query Match
Best Local Similarity 55.7%; Score 39; DB 1; Length 653;
Matches 8; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 PVEKLLPLSL 13
DB 17 PPLPLPLPLSL 27

RESULT 15
RLAO_CAEEL STANDARD; PRT; 311 AA.
ID 093572;
AC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 60S acidic ribosomal protein P0.
DE RPA-0 OR F25H2.10.
GN Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodierinae; Caenorhabditis.
OX NCBI_Taxid-6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RA Wilkinson J.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-15.
RC STRAIN-Bristol N2;
RA Bin L., Heid H., Liberatori S., Geller G., Pallini V., Zwilling R.;
RT "Two-dimensional gel electrophoresis of Caenorhabditis elegans
RT homogenates and identification of protein spots by microsequencing.";
RL Electrophoresis 18:357-362(1997).
-1- FUNCTION: RIBOSOMAL PROTEIN P0 IS THE FUNCTIONAL EQUIVALENT
OF E. COLI PROTEIN L10.
-1- SUBUNIT: P0 FORMS A PENTAMERIC COMPLEX BY INTERACTION WITH
DIMERS OF P1 AND P2.
CC -1- SIMILARITY: BELONGS TO THE L10P FAMILY OF RIBOSOMAL PROTEINS.
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CC
CC EMBL: Z79754; CAB02098.1; -
DR Sienna-2DPAGE: Q93572; -
DR WormPep: F25H2.10; CE09655.
DR InterPro: IPR001813; 60s_ribosomal.
DR InterPro: IPR001790; Ribosomal_L10.
DR Pfam: PF00428; 60s_ribosomal_L10.
DR Pfam: PF00466; Ribosomal_L10; 1.
KW Ribosomal protein; Phosphorylation.
FT INTRAMET 0
SO SEQUENCE 311 AA; 33642 MW; 2FA9A35DCD24DE0F4 CRC64;

Query Match
Best Local Similarity 54.3%; Score 38; DB 1; Length 311;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 NPVEKLLP 10
DB 11:|||||

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Mon Jan 13 09:24:32 2003

handentered.rsp

Page 9

Db 71 NPSLEKLLP 79

Search completed: January 12, 2003, 04:15:39  
Job time : 27 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: January 12, 2003, 02:06:50 ; Search time 80 Seconds

(without alignments)  
36.058 Million cell updates/sec

Title: HANDENTERED

Perfect score: 1 snppvek1plslk 14

Sequence: BLOSUM62

Scoring table: Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SP archaea:\*  
2: SP bacteria:\*  
3: SP fungi:\*  
4: SP human:\*  
5: SP invertebrate:\*  
6: SP mammal:\*  
7: SP mhc:\*  
8: SP organelle:\*  
9: SP phage:\*  
10: SP plant:\*  
11: SP rodent:\*  
12: SP virus:\*  
13: SP vertebrate:\*  
14: SP unclassified:\*  
15: SP virus:\*  
16: SP bacteriophage:\*  
17: SP archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	70	100.0	360	4	09P2Y6
2	47	67.1	889	10	09M1M3
3	43	61.4	213	17	08TUD7
4	42	60.0	209	2	09KW31
5	42	60.0	209	2	09LBD4
6	42	60.0	209	2	056783
7	42	60.0	327	15	066800
8	42	60.0	333	5	P91479
9	42	60.0	366	10	09M259
10	42	60.0	425	16	08R7J8
11	42	60.0	431	4	094800
12	42	60.0	437	11	08VCO4
13	42	60.0	450	10	09CAH1
14	42	60.0	626	4	09NS67
15	42	60.0	653	5	062446
16	42	60.0	916	4	09U1W7

17	42	60.0	1028	4	09URC7	09ufc7 homo sapien
18	42	60.0	1075	10	09LPE2	09lpe2 arabidopsis
19	42	60.0	1350	4	09UPD3	09upd3 homo sapien
20	42	60.0	1544	4	09Y305	09y305 homo sapien
21	42	60.0	1580	4	095811	095811 homo sapien
22	42	60.0	1681	4	09UGL1	09ugl1 homo sapien
23	42	58.6	374	12	09DH06	09dh06 yaba-like d
24	41	58.6	593	16	09PWM3	09pmw3 campylobact
25	41	58.6	649	16	09PMY1	09pmv1 campylobact
26	41	58.6	653	16	09PMW6	09pmw6 campylobact
27	40	57.1	105	16	08W96	08w96 arabidopsis
28	40	57.1	110	12	09Z3F9	09z3f9 arabidopsis
29	40	57.1	320	12	08V3M1	08v3m1 synechococ
30	40	57.1	349	10	09FTT4	09ftt4 oryza sativ
31	39	55.7	315	5	08WQJ2	08wqj2 spodoptera
32	39	55.7	317	4	09BVK4	09bv44 homo sapien
33	39	55.7	317	11	09G154	09g154 mus musculu
34	39	55.7	317	13	090YX1	090yx1 ictalurus p
35	39	55.7	343	13	08W98	08w98 xenopus lae
36	39	55.7	347	5	09GZC7	09gzc7 trypanosoma
37	39	55.7	366	12	09OBC3	09obc3 yaba monkey
38	39	55.7	367	16	09ZNT5	09znt5 rhizobium m
39	39	55.7	442	4	09NUP1	09nut1 homo sapien
40	39	55.7	442	4	08W61	08w61 homo sapien
41	39	55.7	488	16	08U931	08u931 agrobacteri
42	39	55.7	542	12	09LFG3	09lfg3 chilo iride
43	39	55.7	654	11	08VC38	08vc38 mus musculu
44	39	55.7	717	5	09U422	09u422 drosophila
45	39	55.7	799	16	09PDX0	09pdx0 xylella fas

## ALIGNMENTS

RESULT 1  
ID 09P2Y6 PRELIMINARY; PRT; 360 AA.  
AC 09P2Y6; (TREMUR1.15, Created)  
DT 01-OCT-2000 (TREMUR1.15, Last sequence update)  
DT 01-OCT-2000 (TREMUR1.15, Last sequence update)  
DT 01-JUN-2002 (TREMUR1.21, Last annotation update)  
DE Carboxypeptidase B-like protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Matsunoto A.;  
RT "Isolation, molecular cloning, and partial characterization of a novel  
RT carboxypeptidase B from human plasma."  
RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.  
[2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92042093; PubMed=1939207;  
RA Eaton D.L., Malloy B.E., Tsai S., Henzel W., Drayna D.;  
RT "Isolation, molecular cloning, and partial characterization of a novel  
RT carboxypeptidase B from human plasma."  
DR J. Biol. Chem. 266:21833-21838(1991).  
DR EMBL; AB011969; BAA90475.1; -;  
DR HSSP; P00730; ZCTC.  
DR MEROPS; M14.009; -;  
DR InterPro; IPR003146; Propep\_M14.  
DR InterPro; IPR000834; Zn\_carboxypept.  
DR Pfam; PF00244; Propep\_M14.1.  
DR Pfam; PF00246; Zn\_carboxypept; 1.  
DR PRINTS; PR00765; CRHOXPTASEA.  
SQ SEQUENCE 360 AA; 40935 MW; BF670B2F7437C1CB CRC64;

Query Match 100.0%; Score 70; DB 4; Length 360;  
Best Local Similarity 100.0%; Pred. NO. 0.00022;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

*4-identical  
c-term. identical*

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QY 1 SNPPVKLPLSLK 14
DB 347 SNPPVKLPLSLK 360

RESULT 2
ID 09MIM3 PRELIMINARY; PRT; 889 AA.
AC 09MIM3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 100.0 KDa protein.
GN T32A11_100.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN (1)
RP SEQUENCE FROM N.A.
RA Rieger M., Mueller-Auer S., Zipp M., Schaefer M., Nemes H.W., Rudd S.,
RA Lemcke K., Mayer K.F.X., Quettler F., Salanoubat M.;
RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AL138653; CAB85976.1; -.
DR InterPro: IPR001092; SUMO_protease.
DR InterPro: IPR003653; HLH_basic.
DR Pfam: PF02802; Peptidase_C48; 1.
DR PROSITE: PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
KW Hypothetical protein.
SQ SEQUENCE 889 AA; 100009 MW; DBCA359CA9CFF7B CRC64;

Query Match
Best Local Similarity 67.1%; Score 47; DB 10; Length 889;
Matches 9; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SNPPVKLPLSLK 12
DB 552 SNPPVKLPLSLK 563

RESULT 3
ID 08TLD7 PRELIMINARY; PRT; 213 AA.
AC 08TLD7;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Predicted protein.
GN MA3099.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Methanococci; Methanosarcinales;
OC Methanosarcinaceae; Methanosarcina.
OX NCBI_TaxID=2214;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P.,
RA Fitzhugh W., Calvo S., Engels R., Smirnov S., Alnoor D., Brown A.,
RA Allen N., Naylor J., Stange-Thomann N., DeArlellano K., Johnson R.,
RA Litton L., McEwan P., McKernan K., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Grahame D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
RA Leight J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayam L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;

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RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542(2002).
DR EMBL; AF011013; AAM06472.1; -.
KW Complete proteome.
SQ SEQUENCE 213 AA; 24042 MW; 8C7A47C1A28451A CRC64;

Query Match
Best Local Similarity 61.4%; Score 43; DB 17; Length 213;
Matches 6; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 3 PVEKLLPLSLK 14
DB 189 PVEKLLPLSLK 200

RESULT 4
ID 09KW31 PRELIMINARY; PRT; 209 AA.
AC 09KW31;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE HrpB4.
GN HRPB4.
OS Xanthomonas oryzae pv. oryzae.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xanthomonas.
OX NCBI_TaxID=64187;
RN (1)
RP SEQUENCE FROM N.A.
RA STRAIN=MAFF 311018;
RX MEDLINE=21303248; PubMed=11410350;
RA Ochiai H., Inoue Y., Hasebe A., Kaku H.;
RT "Construction and characterization of a Xanthomonas oryzae pv. oryzae
RT bacterial artificial chromosome library.";
RL FEMS Microbiol. Lett. 200:59-65(2001).
DR EMBL; AB045311; BAB07854.1; -.
SQ SEQUENCE 209 AA; 22245 MW; 8320BD30BBD2A429 CRC64;

Query Match
Best Local Similarity 60.0%; Score 42; DB 2; Length 209;
Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 SNPPVKLPLSLK 13
DB 162 SNPPVKLPLSLK 174

RESULT 5
ID 09LBD4 PRELIMINARY; PRT; 209 AA.
AC 09LBD4;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE HrpB4.
GN HRPB4.
OS Xanthomonas oryzae pv. oryzae.
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xanthomonas.
OX NCBI_TaxID=64187;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=PX086;
RX MEDLINE=20179797; PubMed=10714988;
RA Zhu W., Magbanua M.M., White F.F.;
RT "Identification of two novel hrp-associated genes in the hrp gene
RT cluster of Xanthomonas oryzae pv. oryzae.";
RL J. Bacteriol. 182:1844-1853(2000).
DR EMBL; AF026197; AAF61283.1; -.
SQ SEQUENCE 209 AA; 22259 MW; 31D0034EBC35384A CRC64;

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Query Match 60.0%; Score 42; DB 2; Length 209;  
 Best Local Similarity 76.9%; Pred. No. 14;  
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 SNPEKILPLSL 13  
 DB 162 SNPVAKLALSL 174

RESULT 6  
 056783  
 ID 056783 PRELIMINARY; PRT; 209 AA.  
 AC 056783;  
 DT 01-NOV-1996 (TREMblrel. 01, Created)  
 DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE HRPB4.  
 GN HRPB4.  
 OS Xanthomonas campestris (pv. vesicatoria).  
 OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;  
 OC Xanthomonas.  
 OX NCBI\_TaxID=341;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=75-3;  
 RX MEDLINE=96112739; PubMed=8664494;  
 RA Fenselau S., Bonas U.;  
 RT "Sequence and expression analysis of the hrp pathogenicity operon of Xanthomonas campestris pv. vesicatoria which encodes eight proteins with similarity to components of the Hrp, Ysc, Spa, and Flj secretion systems."  
 RL M01. Plant Microbe Interact. 8:845-854(1995).  
 DR EMBL; U33548; AAB08459.1; -;  
 SQ SEQUENCE 209 AA; 22358 MW; CC227C752FB9291 CRC64;

Query Match 60.0%; Score 42; DB 2; Length 209;  
 Best Local Similarity 76.9%; Pred. No. 14;  
 Matches 10; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 SNPEKILPLSL 13  
 DB 162 SNPVAKLALSL 174

RESULT 7  
 066800  
 ID 066800 PRELIMINARY; PRT; 327 AA.  
 AC 066800;  
 DT 01-AUG-1998 (TREMblrel. 07, Created)  
 DT 01-AUG-1998 (TREMblrel. 07, Last sequence update)  
 DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)  
 DE Hypothetical protein A0\_512.  
 GN A0\_512.  
 OS Aquifex aeolicus.  
 OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.  
 OX NCBI\_TaxID=63363;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=VF5;  
 RX MEDLINE=98196666; PubMed=9537320;  
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Sneed M.A., Keller M., Aubay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;  
 RT "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus."  
 RL Nature 392:353-358(1998).  
 DR EMBL; AE000693; AAC06763.1; -;  
 DR InterPro; IPR001485; PG/PMW\_mutase.  
 DR Pfam; PF02878; PGM\_PMM\_1; 1.  
 DR PROSITE; PS00710; PGM\_PMM\_1.  
 KW Hypothetical protein: Complete proteome.  
 SQ SEQUENCE 327 AA; 37884 MW; A2200A1CDD7076C7 CRC64;

Query Match 60.0%; Score 42; DB 16; Length 327;  
 Best Local Similarity 63.6%; Pred. No. 21;  
 Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 SNPEKILPLSL 11  
 DB 311 SNPLPKMFPL 321

RESULT 8  
 P91479  
 ID P91479 PRELIMINARY; PRT; 333 AA.  
 AC P91479;  
 DT 01-MAY-1997 (TREMblrel. 03, Created)  
 DT 01-MAY-1997 (TREMblrel. 03, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE Hypothetical 37.8 kDa protein.  
 GN T20F5.4.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;  
 OC Rhabditidae; Pelodderinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RX MEDLINE=99069613; PubMed=9851916;  
 RA None;  
 RT "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."  
 RL Science 282:2012-2018(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Du Z., Le T.T.;  
 RT "The sequence of C. elegans cosmid T20F5."  
 RL submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BRISTOL N2;  
 RA Waterston R.;  
 RT "Direct Submission."  
 RL submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; U80442; AAB37655.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 333 AA; 37825 MW; 8CF145617A9DC8CD CRC64;

Query Match 60.0%; Score 42; DB 5; Length 333;  
 Best Local Similarity 53.8%; Pred. No. 22;  
 Matches 7; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 2 NPVEKILPLSLK 14  
 DB 272 SPVRRALPLSLK 284

RESULT 9  
 09M259  
 ID 09M259 PRELIMINARY; PRT; 366 AA.  
 AC 09M259;  
 DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-OCT-2000 (TREMblrel. 15, Last annotation update)  
 DE Hypothetical 40.6 kDa protein.  
 GN F7M19.30.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eustosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Nyakatura G., Fartmann B., Dauner D., Steir W., Holland R., Weichselgartner M., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.,

RL	Nat. Biotechnol.	16:1338-1342(1998).
DR	EMBL:	AB015348; BAA34803.1; -
DR	InterPro:	IPR001965; znf_PHD.
DR	Pfam:	PF00628; PHD; 1.
DR	SMART:	SM00249; PHD; 1.
FT	NON_TER	1
SQ	SEQUENCE	431 AA; 48637 MW; 747B327207643996 CRC64;
 Query Match		
Best Local Similarity 60.0%; Score 42; DB 4; Length 431;		
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0		
OY	3 PVEKILPL 11	:
Db	147 PLEKILPL 155	
 RESULT 12		
ID	QBVC04	PRELIMINARY; PRT; 437 AA.
AC	QBVC04;	
DT	01-MAR-2002 (TREMBlrel. 20, Created)	
DT	01-MAR-2002 (TREMBlrel. 20, Last sequence update)	
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)	
DE	Hypothetical 49.2 kDa protein (Fragment).	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxID=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	TISSUE=MAMMARY TUMOR;	
RA	Strausberg R.;	
RL	Submitted (DEC-2001) to the EMBL/Genbank/DDBJ databases.	
DR	EMBL: BC019446; AAA19446.1; -	
DR	InterPro: IPR001965; znf_PHD.	
DR	Pfam: PF00628; PHD; 2.	
DR	SMART: SM00249; PHD; 2.	
KW	Hypothetical protein.	
FT	NON TER	1
SQ	SEQUENCE	437 AA; 49224 MW; FGF0EA766D817E87 CRC64;
 Query Match		
Best Local Similarity 60.0%; Score 42; DB 11; Length 437;		
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;		
OY	3 PVEKILPL 11	:
Db	120 PLEKILPL 128	
 RESULT 13		
ID	O9CAH1	PRELIMINARY; PRT; 450 AA.
AC	O9CAH1;	
DT	01-JUN-2001 (TREMBlrel. 17, Created)	
DT	01-JUN-2001 (TREMBlrel. 17, Last sequence update)	
DT	01-JUN-2002 (TREMBlrel. 21, Last annotation update)	
DE	Hypothetical 50.9 kDa protein.	
GN	F28P22.27.	
OS	Arabidopsis thaliana (Mouse-ear cress).	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;	
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;	
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsids.	
OX	NCBI_TaxID=3702;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=CV. COLUMBIA;	
RA	MEDLINE=21016719; PubMed=11130712;	
RA	Theologis A., Becker U.R., Palm C.J., Federspiel N.A., Kaul S.,	
RA	White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,	
RA	Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,	
RA	Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K	

RA Dunn P., Etgu P., Feldblum T.V., Peng J.-D., Fong B., Fujii C.Y.,  
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,  
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,  
 RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,  
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziani A.,  
 RA Miliescher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,  
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
 RA Sakano H., Salzer S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
 RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,  
 RA Utechtack T., Van Aken S., Vaysberg M., Vysotskaya V.S., Walker M.,  
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.,  
 RT "sequence and analysis of chromosome 1 of the plant Arabidopsis  
 RT thaliana.";  
 RL Nature 408:816-820(2000).  
 DR EMBL: AC010926; AAC51840.1; -;  
 DR InterPro: IPR000719; Euk\_pkinase.  
 DR InterPro: IPR002290; Ser\_thr\_pkinase.  
 DR InterPro: IPR001245; Tyr\_pkinase.  
 DR Pfam: PF00069; pkinase; 1.  
 DR PRINTS: PR00109; TYRKINASE.  
 DR PRODOM: PD000001; Euk\_pkinase; 1.  
 DR SMART: SM00220; S\_TKc; 1.  
 DR SMART: SM00219; TYRKc; 1.  
 DR PROSITE: PS00107; PROTEIN\_KINASE\_ATP; UNKNOWN\_1.  
 DR PROSITE: PS50011; PROTEIN\_KINASE\_DOM; 1.  
 DR PROSITE: PS00108; PROTEIN\_KINASE\_ST; 1.  
 KW ATP-binding; Hypothetical protein; Transferase.  
 SQ SEQUENCE 450 AA; 50875 MW; 847753292B6AF26 CRC64;

Query Match 60.0%; Score 42; DB 10; Length 450;  
 Best Local Similarity 75.0%; Pred. No. 29;  
 Matches 9; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 SNPEKILPLS 12  
 Db 26 TNPKEKILPLS 37

RESULT 14  
 Q9NSZ7 PRELIMINARY; PRT; 626 AA.  
 AC Q9NSZ7;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Hypothetical 70.4 kDa protein (Fragment).  
 GN DKFZP434I2412.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-TESTIS;  
 RA Duesterhoeft A., Lauber J., Mewes H.W., Weil B., Wiemann S.;  
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL137622; CAB70847.1; -;  
 DR InterPro: IPR001965; Znf\_PHD.  
 DR Pfam: PF00628; PHD; 2.  
 DR SMART: SM00249; PHD; 2.  
 KW Hypothetical protein.  
 FT NON\_TER  
 SQ SEQUENCE 626 AA; 70422 MW; 3FE05038C914E22C CRC64;

Query Match 60.0%; Score 42; DB 4; Length 626;  
 Best Local Similarity 77.8%; Pred. No. 41;  
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 PPEKILPL 11  
 Db 309 PPEKILPL 317

RESULT 15  
 062446 PRELIMINARY; PRT; 663 AA.  
 AC 062446;  
 DT 01-AUG-1998 (TREMBlrel. 07, Created)  
 DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)  
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
 DE Y43FA.1 protein.  
 GN Y43FA.1.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;  
 OC Rhabditidae; Pelodierinae; Caenorhabditis.  
 OX NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Matthews L.;  
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-99069613; PubMed-9851916;  
 RA none;  
 RT "Genome sequence of the nematode C.elegans: A platform for  
 RT investigating biology.";  
 RL Science 282:2012-2018(1998).  
 DR EMBL: Z99271; CAB16471.1; -;  
 DR MEROPS: M08.002; -;  
 DR InterPro: IPR001577; Peptidase\_M8.  
 DR InterPro: IPR000130; Zn\_MTpeptidse.  
 DR Pfam: PF01457; Peptidase\_M8; 1.  
 DR PROSITE: PS00142; ZINC\_PROTEASE; UNKNOWN\_1.  
 SQ SEQUENCE 663 AA; 76050 MW; 814C317228B5ACBA CRC64;

Query Match 60.0%; Score 42; DB 5; Length 663;  
 Best Local Similarity 50.0%; Pred. No. 43;  
 Matches 7; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

OY 1 SNPEKILPLSLK 14  
 Db 60 TSPPEKFAPLRIQ 73

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